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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:
August 16, 2004, 09:38:15; Search time 99 Seconds

Title:
Buckers (c) 193
117.015 Million cell updates/sec

Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aag73954 Human col	_	Ade63987 Human Pro	Aay27443 Amino aci	Adc31629 Human nov	Aau30004 Novel hum	Adc31631 Human nov	6 Human	Aab82020 Human hep	Aau33060 Novel hum	Ade54611 Human Pro	Add45108 Human Pro	Abr59727 Human moe	Adb70362 Moesin SE	Adc77532 Human moe	Abg19947 Novel hum	Adb79911 Mouse put		Abg16577 Novel hum	Abu89709 Protein d	Σ	Adc77526 Zebrafish	Abu53290 Human tes	Abu53269 Human tes	Abu53270 Human tes
SUMMARIES	ç	77	AAG73954	ADC31630	ADE63987	AAY27443	ADC31629	AAU30004	ADC31631	AAB53356	AAB82020	90	ADE54611	ADD45108	ABR59727	ADB70362	ADC77532	ABG19947	ADB79911	7	ABG16577	ABU89709	ADC77529	ADC77526	ABU53290	ABU53269	ABU53270
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Abu53286 Human tes	Abu53289 Human tes	Abu53283 Human tes	Abu53282 Human tes	Abu53268 Human tes	. Aaw27161 Mouse rec	Abu53276 Human tes	Abu53279 Human tes	Abu53281 Human tes	Abu53271 Human tes	Abu53274 Human tes	Adb65482 Human pro	Abb71879 Drosophil	Aay30795 A human t	Add48869 Human Pro	Abu53273 Human tes	Abu53277 Human tes	Abu53278 Human tes	Abb58657 Drosophil	Abu53272 Human tes
ABU53286	ABU53289	ABU53283	ABU53282	ABU53268	AAW27161	ABU53276	ABU53279	ABU53281	ABU53271	ABU53274	ADB65482	ABB71879	AAY30795	ADD48869	ABU53273	ABU53277	ABU53278	ABB58657	ABU53272
4	4	4	4	4	7	4	4	4	4,	4	7	4	N	7	4	4	4	4	4
110	115	116	282	357	2707	76	120	135	339	105	650	730	1898	1898	85	105	144	2274	152
40.9	40.9	40.9	40.9	40.9	40.9	39.9	39.9	39.9	39,9	38.9	38.1	37.8	37.8	37.8	37.6	37.6	37.6	37.0	36.8
79	79	79	79	79	79	17	77	77	77	75	73.5	73	73	73	72.5	72.5	72.5	71.5	71
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 AAG73954 ID AAG73954 standard; protein; 436 AA. XX AC AAG73954;	DT 03-SEP-2001 (first entry) . XX	DE Human colon cancer antigen protein SEQ ID NO:4718. XX	KW Human; colon cancer; colon cancer antigen; diagnosis; detection; KW colorectal carcinoma.	XX OS Homo sapiens.	XX PN W0200122920-A2.	AX PD 05-APR-2001.	XX PF 28-SEP-2000; 2000MO-US026524.	AA 29-SEP-1999; 99US-0157137P. PR 03-NOV-1999; 99US-0163280P.	AX (HUMA-) HUMAN GENOME SCI INC.	AA PI Ruben SM, Barash SC, Birse CE, Rosen CA;	DR WPI; 2001-235357/24.	Nucleic acids encoding 4277 human colon cancer-associated polypeptides, PT useful for preventing, diagnosing and/or treating colorectal cancers.	AA. PS Claim 11; Page 6520-6521; 9803pp; English. vv	AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human o	CC cancer-associated nucleic acid molecules (N) and proteins (P), where the CC proteins are collectively known as colon cancer antioens. The colon	cancer antigens have cytostatic	or and treatment of diseases associated with inappropriate expression. For	example, N and P may be used to treat disorders associated with decrea		supplement the patients own production of P. Additionally, N may be	CC to produce the colon cancer-associated Ps, by inserting the nucleic acids CC into a host cell and culturing the cell to express the proteins. N and P	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autolimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q25.2-26,
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Weng G;
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Asundi V, Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 EREKEÇMMREKEELMLRLÓDYEEKTKKAERELSEÇIQRALG 224
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                                                                                                                                                                                                                                                                                                                       99.0%; Score 191; DB 4;
97.6%; Pred. No. 2.7e-13;
live 0; Mismatches 1;
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Wang D, Ma Y, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 97.6
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEO INC.
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                                                                                                                                                                                                                                                           Sequence 436 AA;
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ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 (ADC31861-ADC32627) and the polyneptides encoded by the invention are allocated in diagnostics, drug screening, forenasts, deme mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet ancers, and in the recombinant production of a protein. The polypeptides are also used using many also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptide are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence of the invention. As sequence of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%; Score 191; DB 7; Length 579; 97.6%; Pred. No. 3.7e-13; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE63987 standard; protein; 585 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page; 1017pp; English
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 97.6
Les 40; Conservative
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New composition for prevention and treatment of tumors and metastasis.

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The invention discloses a composition comprising two or more isolated rate or human polymuclectides or a polymuclectide which represents a fragment, derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the movel polymuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates to the expression of a polymuclectide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the regulates the activity of one or more of the regulates the activity of one or more of the polymuclectides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polymeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating to modulates its activity is useful for preparing a medicament for treating conjury (CI) and spared nerve injury (CMUM), chronic construction injury (CI) and spared nerve injury (SNUM) in an animal (e.g. spin) endered nerve injury (SNUM) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed composition compressed the printed specification, but was obtained in electronic form directly from WIPO at Epp.
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.. 0 Gaps ; 0 Score 191; DB 7; Length 585; Pred. No. 3.7e-13; 0; Mismatches 1; Indels 333 EREKEÇMMREKEELMLRLQDYEEKTKKAERELSEQIQRALQ 373 1 EREKEOMMREKEELMIRLODXEEKTKKAERELSEQIORALO 41 99.0%; 40; Conservative Local Similarity Query Match ð

Amino acid seguence of human ezrin polypeptide. AAY27443 standard; protein; 586 AA (first entry) 26-NOV-1999 Homo sapiens AAY27443; RESULT 4

/note= "the Tyr at this position can be mutated (preferably to a Phe) to construct an ezrin mutant of the invention" Pharmaceutical; ezrin; mutant; tumor; metastasis; human. Location/Qualifiers Misc-difference

WO9947150-A2

99WO-EP002054 18-MAR-1999; 23-SEP-1999,

98US-00040725 18-MAR-1998; (CURI-)

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ñ Louvard Gautreau A, Crepaldi T, WPI; 1999-561851/47 Arpin M,

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                                                                                The invention provides a pharmaceutical composition containing ezrin protein, RNA or DNA mutated on tyrosine 353, or a functional fragment or derivative of the ezrin mutant. The new composition is useful for prevention and/or treatment of tumors, and especially metastasis. The present sequence represents the amino acid sequence of human ezrin (before the maturation by deletion of the first amino acid Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neucodegenerative disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q25.2-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the
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Wang Z, W
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Y, Asundi V,
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Wang D, Ma Y,
                                                 Example 1; Fig 1; 31pp; English.
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                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang TY, Zhang J,
Zhou P, Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
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                                                                                                                                                                                                      Sequence 586 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC31629;
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                        Matches
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recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting of polymucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or methods of invention methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the cortis sequences corresponding to the cDNs sequences of the invention (ADC31861-ADC32627) and the polymucleotide and/or polypeptides of the invention cortis sequences corresponding to the cDNs sequences of the invention (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628 consected in diagnostics, drug sare enabling, forensics, gene mapping, in the cuseful in diagnostics, drug screenling, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other creating diseases such as Parkinson's disease, Alzheimer's also used for treating diseases such as Parkinson's disease, Alzheimer's cancer. The nucleic acids may also be used as hybridisation probes or chiners, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and and propered esquence of the invention. Note: The sequence cancer the patent did not form part of the printed specification, but contained in the recombinant diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained in electronic format directl
ftp.wipo.int/pub/published_pct_sequences.
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Gaps ; 0 Length 611; 1; Indels 41 1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEQIORALO Match 99.0%; Score 191; DB 7; Local Similarity 97.6%; Pred. No. 3.9e-13; les 40; Conservative 0; Mismatches 1; Query Match Best Loca Matches δ

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334 EREKEÇIMMREKEELMIRLQDYEEKTKKAERELSEQIQRALQ 374

RESULT 6 AAU30004

AAU30004;

AAU30004 standard; protein; 622

(first entry) 18-DEC-2001 Novel human secreted protein #495

Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune suppression, immune stimulation, anti-inflammatory, leukaemia.

Homo sapiens.

WO200179449-A2

25-OCT-2001

16-APR-2001; 2001WO-US008656

18-APR-2000; 2000US-00552929 26-JAN-2001; 2001US-00770160

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT,

WPI; 2001-611725/70.

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.

cancer.

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated at the latered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberran expression or physiological interactions of the polypeptide. Vectors comprising the consists and are also useful for producing the proteins in the early of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of are useful in genetic vaccination, testing and therapy, and can be used as untritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and profession and/or are assimilation, as anti-inflammatory agents, and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human are considered proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; hardenerive disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimune disease; carcer; molecular weight marker; food supplement; antiparkinsonian; notropic; autoimune disease; antiensian; osteopathic; antiensemic; anticoagulant; thrombolytic; vulnerary; antitucer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q25.2-26.
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Wang D, Ma Y, Asundi V, Wang Z, Weng G;
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Pred. No. 4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel polypeptide sequence, SEQ ID NO:1713.
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Claim 20; Page 219; 765pp; English.
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Ghosh M, Y
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Zhou P, G
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Matches
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                                                                                           The invention relates to 91 nover name cure sequences (ADC291960). The invention also relates to nucleic acid sequences over 93% identical with the nover numen context invention and difficulally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; a method of detecting against a polypeptide of the invention; a method of detecting polymucleotides or polypeptides of the invention; and methods of invention further discloses methods of peventing, treating or invention further discloses methods of peventing, treating or medical condition; kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the invention; methods for the polymucleotide and/or polypeptide; and 767 conting sequences corresponding to the conting sequences corresponding to the conting sequences corresponding to the conting sequences of the invention are useful in diagnostics, during screening, forensics, gene mapping, in the identification of mucations responsible for genetic disorders or other craits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's allaber's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fix. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identífication; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                invention relates to 971 novel human cDNA sequences (ADC29919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease and other neurodegenerative diseases, anaemia, platelet
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Pred. No. 4e-13;
0; Mismatches 1; Indels
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                            Claim 20; SEQ ID NO 1713; 1185pp; English.
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Local Similarity 97.6%;
Les 40; Conservative 0
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Matches
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, reproductive disorders, and cardiovascular disorders, infectious diseases, and cardiovascular disorders, and the present invention represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; hepreceptor domain B; cytostatic; anti-HIV; antibiotic; nootropic; immune response inducer; ezrin; infectious diseases; cancer;
                                                                                                                                                                                                                                                                                            Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1449-1451; 2104pp; English.
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                                                                                                                                                                                                                                                                                                                               antigens, useful for the treatm
disorders such as colon cancer.
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                                                               (HUMA-) HUMAN GENOME SCI INC.
12-MAR-1999; 99US-0124270P
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Best Local Similarity 97.6
Matches 40; Conservative
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                                                                                                                                 Ruben SM;
                                                                                                                                                                                                 WPI; 2000-587534/55.
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D.
                                                                                                                                                                                                                                N-PSDB; AAC98113.
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Modified-site
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                                                                                                                                     Rosen CA,
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The present sequence is domain B of human hepreceptor of human ezrin. The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AAB82021 to AAB82041) that bind to hepreceptor with greater affinity than HEP1 (see immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present sequence assembles into two anti-parallel helices with hepreceptor domain A (see AAB82019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel human secreted polypeptides. The polypeptides are useful for polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at therapeutic agent for use in treatment of a pathology related to aberrant expression or
                                             Novel regulatory or unfolding peptides of ezrin that binds to
Hepreceptor, useful for inducing immune response for treating infectious
diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                      80.8%; Score 156; DB 4;
97.1%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MREKBELMLRLQDYEBKTKKAERELSEQIQRALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted protein #3551.
                                                                                                                      Claim 5; Page 36; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU33060 standard; protein; 52
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26-JAN-2001; 2001US-00770160
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Best Local Similarity 97.1;
Matches 33; Conservative
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               WPI; 2001-293287/31
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                                                                                                                                                                                                                                                                                                                                        Sequence 34 AA;
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AAU33060
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physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29910.AAU3334 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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                                                                                                                                                                                                                                                                     Query Match
11.5%; Score 138; DB 4;
Best Local Similarity 78.4%; Pred. No. 2.2e-08;
Matches 29; Conservative 3; Mismatches 5.
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                                                                                                                                                                                           secreted proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-268312/26
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                                                                                                                                                                                                                                   Sequence 52 AA;
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41

Length 34; Indels

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25-JUL-2003
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Best Local S
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compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypetides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CMI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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Pred. No. 3e-06;
9; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Protein P26038, SEQ ID NO 10541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD45108 standard; protein; 576 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 63...

Local Similarity 63...

Local Similarity 63...
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                                                                                                                                                                                                                                                                   Sequence 576 AA;
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that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polymetic composition, a method for identifying a compound useful in treating companies or their antibodies. The polymucleotide or the compound that polymeptides or their antibodies. The polymucleotide or the compound that compliant (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene continguation) which is differentially expressed during pain. Note: The sequence data for this parent did not form part of the printed contingual contingu
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Pred. No. 3e-06;
9; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 107-108; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-363276/34.
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The invention relates to a novel method for identifying a compound that modulates T lymphocyte activation. The method comprises contacting a T cell comprising an A-raf-1 or TCPTP/PPTNZ polypeptide with a compound, where the A-raf-1 or TCPTP/PPTNZ polypeptide by a nucleic acid that hybridises to a nucleic acid encoding a polypeptide having a sequence selected from two 606-amino acid sequence and 415-amino acid sequence selected from two 606-amino acid sequence and a variant or modulation has immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory activity. The method is useful for identifying compounds that modulate immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory activity. The method is useful for identifying compounds that modulate Immunosuppression and differentiation, and for monitoring changes in cell surface marker expression, cytokine production, antibody production, proliferation and differentiation, and apoptosis, using either cell lines or primary cells. The A-raf-1 or TCPPP/PPNZ proteins may be used as crivation and migration, e.g. for the treatment of diseases in which modulation of the immune response is desired such as delayed type modulation of the immune response is desired such as delayed type confluence and chronic inflammation. Modulators of lymphocyte activation and acute and chronic inflammation. Modulators of lymphocyte activation and chronic inflammation. Modulators of lymphocyte activation and chronic inflammation. The present sequence is used in the exemplification of the
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Match 66.8%; Score 129; DB 6; Length 577; Local Similarity 63.4%; Pred. No. 3e-06; es 26; Conservative 9; Mismatches 6; Indels
                                                                                                                                     1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEOIORALO 41
Sequence 577 AA;
                                     Query Match
                                                          Best Loca
Matches
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Gaps

; 0

ADB70362 standard; protein; 577 (first entry) Moesin SEQ ID NO:54. 04-DEC-2003 ADB70362; ADB70362

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RESULT 14

cancer; malignant pleural mesothelioma; MPM; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;

Homo sapiens.

WO2003021229-A2.

05-SEP-2002; 2002WO-US028203 13-MAR-2003

(BGHM) BRIGHAM & WOMENS HOSPITAL INC.

05-SEP-2001; 2001US-0317389P 30-AUG-2002; 2002US-00236031.

Bueno R; Gullans SR, Gordon GJ, Jensen RV,

WFI; 2003-290233/28. N-PSDB; ADB70361.

Diagnosing cancer cells in tissue sample, or determining prognosis or outcome of cancer patient, by calculating ratio of expression levels of genes that are differentially expressed in cancer and non cancer tissues.

Claim 77; Page 263-264; 396pp; English.

The present invention describes a method (M1) for diagnosing the presence

The present invention describes an isolated nucleic acid (I) comprising:

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the prognosis or non-cancer cells in a tissue sample, or determining the prognosis or outcome of a cancer patient. M1 involves providing a set of genes that are differentially expressed in cancerous or non-cancerous conditions, determining the expression levels of the set of genes and calculating a ratio of the expression levels of the differentially expressed genes. M1 is useful for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, where the cancer is malignant pleural mesotheliona (MPM), lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell prognosis or outcome of a cancer patient. The ratio of expression levels of differentially expressed genes is used as an indicator of cancer type, cancer class, and/or cancer prognosis, all of which are useful for determining a course of treatment of a patient. The present sequence represents a human protein which is used in an example from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid useful for diagnosing, preventing or treating diseases associated with aberrant vascular activity, angiogenesis, vasculogenesis and cartilage or bone formation, e.g. atherosclerosis or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridisation; testicular tumour differentially expressed gene 1; TDE1; patchy vessel; PTV; HLA class II region expressed gene 4; HER4; vascular endothelial growth factor; VEGF; antirheumatic; antiarthritic; antiarteriosclerotic; antidabetic; ophthalmological; antiarchic; cytostatic; osteopathic; antiangiogenic; antisense gene therapy; aberrant vascular activity disorder; andiogenesis; vasculogenesis; cartilage formation disorder; bone formation disorder; rheumatoid arthritis; atherosclerosis; diabetes; retinopathies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wadman S, Essner J, Larson J, Clark KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  66.8%; Score 129; DB 7; Length 577; 63.4%; Pred. No. 3e-06; ive 9; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 27; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC77532 standard; protein; 577 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human moesin protein SEQ ID NO:27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis; cancer; human; moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DISC-) DISCOVERY GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2003; 2003WO-US003747.
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Roberg-Perez S, Ekker SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADC77530, ADC77531.
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Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                  Sequence 577 AA;
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                                                                                                                                                                                                                                                                                                                 nvention.
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the probabilities under stringent conditions to a hybridisation probe comprising a sequence of 1422 (human (testicular) tumour differentially expressed gene I (TDEI) encoding CDNA ADC77521).

786 (human patchy vessels (PTV) encoding CDNA ADC77521) or 1410 (human patchy vessels (PTV) encoding CDNA ADC77521) or 1410 (human patchy vessels (PTV) encoding CDNA ADC77521) or 1410 (human patchy vessels (PTV) encoding CDNA ADC77531) base pairs (bp), or the complement; or (b) a sequence that is 90% identical to the probe sequences or their complements. Also described: (1) a sequence that is at least 8 residues in length and is 90% identical to any of the composition comprising; (a) an isolated polypeptide comprising a sequence that is at least 8 residues in length and is 90% identical to any of the carrier, vascular endothelial growth factor (VBGF) and TDEI or PTV; (2) an antisense polymucleic acid comprising a sequence, where the antisense polymucleic acid suppresses the expression of a human, mouse or zebrafish TDEI, PTV or HKE4; and (3) a teleost comprising the antisense polymucleic acid suppresses the expression of a human, mouse or zebrafish TDEI, PTV or HKE4; and (3) a teleost comprising the antisense polymucleic and antisense polymucleic acid suppresses the expression of a nutisense gene therapy. The nucleic acid (1) and polypeptide encoded by it, can be used for anticible contain or treating diseases or disorders associated with aberrant consecution. The diseases may include rheumatoid arthritis, catheroscierosis, diabetes, retunopathies, psoriasis or cancer. The comparison of the present invention. Sequence 577 AA;

Gaps ·. Query Match 66.8%; Score 129; DB 7; Length 577; Best Local Similarity 63.4%; Pred. No. 3e-06; Matches 26; Conservative 9; Mismatches 6; Indels

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334 EKEKEKIEREKEELMERLKQIEEQTKKAQQELEEQTRRALE 374 DP ò

1 EREKEOMMREKEELMIRLODXEEKTKKAERELSEOIORALO 41

Search completed: August 16, 2004, 09:43:46 Job time : 100 secs

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Appl Appli A

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APPLICANT: CNES
APPLICANT: CNES
APPLICANT: CNES
APPLICANT: CNES
APPLICANT: Crepaldi, Monique
APPLICANT: Crepaldi, Taziana
APPLICANT: Gautreau, Alexis
APPLICANT: Gautreau, Alexis
APPLICANT: Gouvard, Daniel
TITLE OF INVENTION: Parmaceutical composition containing ezrin mutated
TITLE OF INVENTION: no tyroscine 353
FILE REFERENCE: 391082000100
FILE REFERENCE: 391082000100
CURRENT PRILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Lee, Seung-Chul
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyul
APPLICANT: Chung, Soo-11
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
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US-09-154-750A-85
US-09-665-479A-12
US-09-595-684B-23
US-09-595-084-2
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US-08-655-479A-14
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Pred. No. 5.7e-14;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09040725A; Patent No. 6399584; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 99.0%;
1 Similarity 97.6%;
40; Conservative (
     TYPE: PRT
CORGANISM: Homo sapiens
US-09-040-725A-1
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Sequence 6436, Appl
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                                                                                                               August 16, 2004, 09:45:46; Search time 19 Seconds (without alignments) 111.403 Million cell updates/sec
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Sequence 15
Sequence 15
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                    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-261-258-580
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US-09-177-431-2
US-09-177-431-2
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US-09-208-568-2
US-09-208-568-2
US-09-410-399-2
US-08-467-781-4
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US-09-370-838-193
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Gaps

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GENERAL INFORMATION:
APPLICANT: GRAY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI)
TITLE OF INVENTION: UDAGMOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US (99/543, 681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6436
LENGTH: 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                              Query Match

37.8%; Score 73; DB 2; Length 1898;
Best Local Similarity 41.2%; Pred. No. 3.2;
Matches 14; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZOOD7P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT RILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                               2 REKEÇMMREKEELMLRLQDXEEKTKKABRELSEQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 4
Pred. No. 7;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.09-543-681A-6436
Sequence 6436, Application US/09543681A
Patent No. 6605709
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APPLICATION NUMBER: 60/048,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 580, Application US/09205258 Patent No. 6525174
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                  TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0-90-266
(714) 760-0404
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Best Local Similarity 43.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Proteus mirabilis
                                                                                                                    TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800-644-94
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  TELEPHONE:
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US-09-205-258-580
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APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, So-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
CORRESPONDENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 37.8%; Score 73; DB 1; Length 1898; Best Local Similarity 41.2%; Pred. No. 3.2; Matches 14; Conservative 10; Mismatches 10; Indels
                                                                                          COMPUTER TELODOY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FRETATION NUMBER: 36,799
REGISTRATION NUMBER: MIH054.001A
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION OF 304:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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SOFTWARES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1997
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/056,200
APPLICATION NUMBER: US 08/056,200
APPLORATION NUMBER: US 08/056,200
APPLORATION NUMBER: WARE WARES FEATICK, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 REKEOMMREKEELMLRLODXEEKTKKAERELSEQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/08800644
Patent No. 5958752
GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1898 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Newport Beach
CA
U.S.A.
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                               COUNTRY: U
ZIP: 92660
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BARLIER PELING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,085
EARLIER APPLICATION NUMBER: 60/048,084
EARLIER APPLICATION NUMBER: 60/048,094
EARLIER APPLICATION NUMBER: 60/048,994
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PERING DATE: 1997-06-06
EARLIER PERING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER PILING DATE: 1997-06-06
EARLIER
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| Owery Match | Sit 49, Scote 67.5; DB 4; Length 64; | | | | |
| Dest Local Similarity | 33.54; | Pred, No. 0.38; |
| Matches | 15, Concervative | 10; Mismatches | 10; Indels | 3; daps |
| Dest Local Similarity | 33.54; | Pred, No. 0.38; |
| Dest Elecal Similarity | 33.54; | Pred, No. 0.38; |
| Dest Elecal Similarity | 33.54; | Pred, No. 0.38; |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | 10; | Indels | 3; daps |
| Dest Elecal Similarity | 10; | Indels | Indels | 10; | Indels |
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Sequence 4, Application US/09177431

Patent No. 6071700:
GENERAL INFORMATION:
APPLICANT: He, Feng
APPLICANT: He, Feng
APPLICANT: Hachson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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34.2%; Score 66; DB 3; Length 764;
Best Local Similarity 44.4%; Pred. No. 7.4;
Matches 16; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 764; 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
FILLING DATE:
PRIOR ADDATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 1
Pred. No. 7.4;
6; Mismatches
NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEFAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07917/050001
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APPLICATION NUMBER: 08/955,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.4%;
Matches 16; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617/42-986
TELEY. 200154
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-375-300-4
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STATE: MA
COUNTRY: USA
TD: 02110-2804
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US-09-177-431-4
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APPLICANT: Bracobson, Allan S.

APPLICANT: Jacobson, Allan S.

APPLICANT: Jacobson, Allan S.

APPLICANT: Jacobson, Allan S.

APPLICANT: Jacobson, Allan S.

TITLE OF INVENTION: HETEROLOGGUS POLYPEPTIDE PRODUCTION IN

TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION

VINDER OF SEQUENCES:

AUMBER OF SEQUENCES:

AUGUST ALSO SECUENCES:

AUGUST ALSO SECUENCES:

AUGUST AUGUST ALSO SECUENCES:

AUGUST AUGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (409)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-205-258-573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
35.0%; Score 67.5; DB 4; Length 567;
Best Local Similarity 39.5%; Pred. No. 3.7;
Matches 15; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 ERAKEREKRKEQ---EBEEGKEREKEAERERNROLER 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                    EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PATENTING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO S73
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/375,300 FILING DATE: 20-JAN-1995 ATTORNEY/AGENT INFORMATION:
              60/048,917
                                         FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08375300 Patent No. 5679566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-08-375-300-4
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Matches
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Score 66; DB 1; Length 1089;
Pred. No. 11;
6; Mismatches 12; Indels
                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       950 EMKRMYEEYERKLKDEEE--RKAEEELERQFOKMMO 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA.

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTERO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 OMMREKEELMLRLODXEEKTKKAERELSEQIORALQ 41
                                                                                                                                                                                                                                                      NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEPHONE: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/955,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0791
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1089 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.4
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-375-300-2
                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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Patent No. 5579566
CENERAL INFORMATION:
APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: HET ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 5; Length 764;
Pred. No. 7.4;
                                                                                                                                             Sequence 4, Application PC/TUS9516930
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE
TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
TITLE OF INVENTION: PUNCTION
TITLE OF INVENTION: FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FLORDY disk
COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FGSSC, J. PELCI
REGISTRATION NUMBER: 32,993
REGISTRATION NUMBER: 32,993
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 04020/046W01
TELERDANINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 OMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
6 OMMREKEELMLRLODXEEKTKKAERELSEGIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                 3: Fish & Richardson
225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE
TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.4%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 764 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                               STREET: ZZZZZTWY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                          RESULT 9
PCT-US95-16930-4
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US-08-375-300-2
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Gaps

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Sequence 5, Application US/08257073 Patent No. 5766597 GENERAL INFORMATION:
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US-09-134-000C-6355
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                                                                                                                                                                      Score 66; DB 3; Length 1089;
Pred. No. 11;
6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.2%; Score 66; DB 5; Length 1089; Best Local Similarity 44.4%; Pred. No. 11; Matches 16; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
TITLE OF INVENTION: HETEROLOGOUS POLYBERTIDE
TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
TITLE OF INVENTION: NONSENSE-MEDIATED MENA DECAY
TITLE OF INVENTION: FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           950 EMKRMYEEYERKLKDEEE--RKAEEELERQFQKMMQ 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 OMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04020/046WO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELLING DATE: 10.-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046WC
TELECHONE: (617)542-5070
TELEFAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9516930 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
**TWATH: 1089 = mino acids
                                                                                                                                                                        Query Match 34.2%;
Best Local Similarity 44.4%;
Matches 16; Conservative (
                          SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acid
           INFORMATION FOR SEQ ID NO:
                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arent: STREET: Bogton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-16930-2
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RESULT 13 US-08-257-073-5

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Sequence 6355, Application US/09134000C

Patent No. 6617156

CENERAL INFORMATION:

CENERAL INFORMATION:

TITLE OF INVENTION:

THEREPERORM

THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                      SCHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073 FILING DATE: US/08/257,073 CIASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENE/DCOKET NUMBER: 454310-2570
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                            SEE: Curtis, Morris & Safford,
1: 530 Fifth Avenue, 25th Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-UUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-UUN-1993
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                          STATE: New York
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 840-071
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                           Squence 2, Application US/08728323A; Squence 2, Application US/08728323A; Patent No. 5948676; GENERAL INPORMATION:
APPLICANT: Changy Yuan APPLICANT: Bohenaky, Roy A. APPLICANT: Belman, Isidore S. APPLICANT: Belman, Isidore S. APPLICANT: Moore, Patrick S. TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.9%; Score 65.5; DB 2; Length 1162; 37.8%; Pred. No. 13; . tive 11; Mismatches 9; Indels 3.
                                                                                                                         Query Match
33.9%; Score 65.5; DB 4; Length 818;
Best Local Similarity 39.0%; Pred. No. 9.1;
Matches 16; Conservative 10; Mismatches 4; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:::::||||:
46 ERQNLQQQKEELL-----EKKAKQAEQETVIERLKEQIQQ 80
                                                                                                                                                                                          3 EKEÇMMREKEELMLRLQDXEEKTKKAERE----LSEQIOR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQ 37
                                                              TYPE: PRT; ORGANISM: Enterococcus faecalis
US-09-134-000C-6355
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6355
LENGTH: 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 37.8<sup>th</sup>
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-728-323A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                        RESULT 15
US-08-728-323A-2
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Search completed: August 16, 2004, 09:46:37 Job time : 20 secs

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Sequence 4728, Apponence 117, Apponence 117, Apponence 1272, Apponence 160, Apponence 186, Apponence 17, Apploaguence 27, Apploaguence 27, Apploaguence 453, Apploaguence 187, Apploaguence 151, Apploaguence 151,
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Sequence 187, App
Sequence 151, App
Sequence 21, Appl
Sequence 24, Appl
Sequence 32544, A
                                                                                                                                                                         August 16, 2004, 09:49:27 ; Search time 46 Seconds (without alignments) 279.805 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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1 BRSKEQMMREKEBLMLRLQD......BEKTKKAERBLSEQIQRALQ
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| Cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO7 NSW PUB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO7 NSW PUB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO8 NSW PUB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO8 NSW PUB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
| Cgn2 6/ptodata/2/pubpaa/USO08 PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-116-275-117

6 US-10-408-765A-1372

6 US-10-408-765A-1160

US-09-925-29-896

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6 US-10-408-765A-453

6 US-10-408-765A-454

6 US-10-60-849A-21

5 US-10-60-849A-21

5 US-10-60-849A-24

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6 US-10-029-386-32544
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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16 74.5 38.6 621 15 US-10-108-260A-4409 Sequence 4409, Ap 17.5 38.1 650 15 US-10-104-04-3636 Sequence 165506, 12.2 12.0 US-10-108-260A-4344 Sequence 165506, 12.2 12.0 12.0 US-09-789-390-13 Sequence 4344, Appli 22 70.5 36.5 1295 10 US-09-789-390-30 Sequence 30, Appli 22 70.5 36.5 1295 10 US-09-789-390-34 Sequence 31, Appli 22 70.5 36.5 1295 10 US-09-789-390-34 Sequence 31, Appli 22 70.5 36.5 1295 10 US-09-789-390-34 Sequence 32, Appli 22 70.5 36.5 1295 10 US-09-789-390-34 Sequence 31, Appli 22 70.5 36.5 1295 10 US-09-789-390-34 Sequence 31, Appli 22 70.5 36.5 1295 10 US-09-789-390-39 Sequence 31, Appli 22 70.5 36.5 1295 10 US-09-789-390-39 Sequence 31, Appli 32 70.5 36.5 1295 10 US-09-789-390-39 Sequence 31, Appli 32 70.5 36.5 1303 10 US-09-789-390-39 Sequence 35, Appli 33 0.5 1303 10 US-09-789-390-39 Sequence 35, Appli 34 69.5 36.5 1303 10 US-09-789-390-39 Sequence 25, Appli 36.5 1303 10 US-09-789-390-35 Sequence 25, Appli 36.5 1303 10 US-09-789-390-35 Sequence 25, Appli 36.5 1303 10 US-09-789-390-39 Sequence 25, Appli 36.5 1303 10 US-09-789-390-35 Sequence 25, Appli 36.5 1303 10 US-09-789-390-35 Sequence 265, Appli 36.5 135.5 135.5 US-10-104-04-72-3063 Sequence 265, Appli 46.5 15.5 US-10-108-260-314 Sequence 2035, Appli 46.5 15.5 US-10-108-260-314 Sequence 265, Appli 46.5 15.5 US-10-108-260-314 Sequence 265, Appli 47.5 15.0 US-09-933-767-580 Sequence 580, Appli 47.5 15.0 US-09-933-767-580 Seque

ALIGNMENTS

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Sequence 4728, Application US/10106698

Publication No. US20030109690A1

Publication No. US20030109690A1

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

FILE REPERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR FILING DATE: 12000-09-28

FRIOR FILING DATE: 1999-09-29

FRIOR FILING DATE: 1999-09-29

FRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 4728

LINGTH A736

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LINGTH A736
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LOCATION: (382)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino

US-10-106-698-4728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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40; Conserv
US-10-106-698-4728
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Best Local S
Matches 40
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184 EREKEQMMREKEBLMLKLQDYEEKTKKAERELSEQIQRALQ 224

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RESULT 2

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Gaps
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              APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Chosh, Soumitra S.
APPLICANT: Chang, Bind
APPLICANT: Taylor, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Cary M.
APPLICANT: Glenn, Interpretation of the control of the 
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Patent No US20020055627A1
GENERAL INCORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPRENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 100990-03-12
NUMBER OF SEQ ID NOSS: 1556
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
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99.0%; Score 191; DB 16;
Best Local Similarity 97.6%; Pred. No. 5.4e-12;
Matches 40; Conservative 0; Mismatches 1;
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Pred. No. 5.4e-12;
0; Mismatches 1;
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Best Local Similarity 97.6%;
Matches 40; Conservative
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; LENGTH: 635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
SENERAL INFORMATION:
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US-09-925-299-896
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US-09-925-299-896
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                                                                                                   GENERAL INFORMATION:

APPLICANT: Bland Pharmaceutical Technology

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Byrn: Daried

APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Generic Analysis of Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches

TITLE OF INVENTION: Compositions Targeting Peyer's Patches

TITLE OF INVENTION: Compositions Targeting Peyer's Patches

MURBER OF SEQ ID NOS: 349

SEQ ID NOS: 349

SEQ ID NOS: 349

LENGTH: 586

LENGTH: 586
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99.0%; Score 191; DB 15; Length 586;
Best Local Similarity 97.6%; Pred. No. 5e-12;
Matches 40; Conservative 0; Mismatches 1; Indels
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99.0%; Score 191; DB 16; Length 586;
Best Local Similarity 97.6%; Pred. No. 5e-12;
Matches 40; Conservative 0; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2372
LENGTH: 586
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-10-408-765A-2372
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US-10-408-765A-1160
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APPLICANT: Fahy, Edin D.
APPLICANT: Fahy, Edin D.
APPLICANT: Tahy, Edin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Grant Gary M.
APPLICANT: Marnock, Dale B.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME FILE REFERENCE: 660084.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT PILLING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE PARLSEQ for Windows Version 4.0
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APPLICANT: Tang, Enno.
APPLICANT: Taylor, Stander W.
APPLICANT: Taylor, Staven W.
APPLICANT: Taylor, Staven W.
APPLICANT: Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE REPERRACE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 454
LENGTH: 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 453, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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Best Local Similarity 63.43
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 453
LENGTH: 577
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                   LENGTH: 577

TYPE: PRT

CRGANISM: homo sapiens
US-10-360-849A-27
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Publication No. US2003022249A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hackett, Perry
APPLICANT: Hackett, Perry
APPLICANT: Hackett, Jeffrey
APPLICANT: Larson, Jeffrey
APPLICANT: Larson, Jon
APPLICANT: Larson, Jon
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Nadman, Sharnon
APPLICANT: Wadman, Sharnon
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Pred. No. 5.4e-12;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54, Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
APPLICANT: Gualina, Steven No.
APPLICANT: Gualina, Steven R.
APPLICANT: Gualina, Steven R.
APPLICANT: Gualina, Steven R.
APPLICANT: Gualina, Steven R.
APPLICANT:
SHIGE REFERENCE: B08001/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT PILING DATE: 2002-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
66.8%; Score 129; DB 15;
Best Local Similarity 63.4%; Pred. No. 1.5e-05;
Matches 26; Conservative 9; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR FILING DATE: 2001-09-05
PRIOR PELING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
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PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1556 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 896 LENGTH: 635
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Best Local Similarity 97.6%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-925-299-896
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US-10-360-849A-27
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US-10-236-031B-54
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SEQ ID NO 54
LENGTH: 577
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us-09-856-070b-29.std.rapb

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Hackett, Perry
APPLICANT: Nasevicius, Aidas
APPLICANT: Nasevicius, Aidas
APPLICANT: Clark, Karl
APPLICANT: Clark, Karl
APPLICANT: Clark, Karl
APPLICANT: Ekker, Stephen
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Wadman, Shanon
TITLE OF INVENTION: PACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
TITLE OF INVENTION NUMBER: US/10/360,849A
CURRENT FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
LENGTH: 579
TTYPE: NUMBER OF SEQ ID NOS: 72
LENGTH: 579
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APPLICANT: Hackett, Perry
APPLICANT: Basevicius, Aidas
APPLICANT: Basener, Jeffrey
APPLICANT: Basener, Jeffrey
APPLICANT: Basener, Jeffrey
APPLICANT: Larson, Jon
APPLICANT: Larson, Jon
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Medman, Shannon
APPLICANT: Medman, Shannon
TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION, TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
FILE REFERENCE: 3021-055602
CURRENT APPLICATION NUMBER: US/10/360,849A
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: US 60/354,978
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 72
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                                        334 EKEKERIEREKEELMERLRQIEEQTVKAQKELEEQTRKALE 374
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1 EREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.1<sup>3</sup>
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: danio rerio
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LENGTH: 579
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Publication No. US20040106132A1
GENERAL INFORMATION:
PAPPLICATION
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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FILE REFERENCE:
D0273 NP
CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT PILING DATE:
2003-08-26
PRIOR APPLICATION NUMBER:
60/406,385
PRIOR PILING DATE:
2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE PATENTIN Version 3.2
SEQ ID NO 187
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| Sequence 151, Application US/10205219
| Publication No. US2030138803A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Warner-Lambert Company
| APPLICANT: Dixon, Alistair
| APPLICANT: Dixon, Alista
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                                                                                                           Query Match 66.8%; Score 129; DB 16; Length 577; Best Local Similarity 63.4%; Pred. No. 1.5e-05; Matches 26; Conservative 9; Mismatches 6; Indels (
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CORGANISM: Homo sapiens
US-10-648-593-187
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   ; ORGANISM: Homo sapiens
US-10-408-765A-454
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Sequence 325444

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SEQUENCE 32644

SEQUENCE 3206-3264

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Query Match 60.6%; Score 117; DB 15; Length 579; Best Local Similarity 56.1%; Pred. No. 0.00026; Matches 23; Conservative 12; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRGANISM: Homo sapiens
CRGANISM: Homo sapiens
FEATURE:
CTHER INFORMATION: MAP TO ACCIO474.2
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.1
CTHER INFORMATION: SWISSPROT HIT: P26038, EVALUE 2.00e-97
US-10-029-386-32544
                                                                                                                       1 BREKEOMMREKEELMLRLQDXEEKTKKAERELSEQIORALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EREKEQMMREKBELMLRLQDXEEKTKKAERELSEQ 35
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Job time : 46 secs
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OM protein - protein search, using sw model

Run on:

August 16, 2004, 09:44:16; Search time 16 Seconds (without alignments) 246.491 Million cell updates/sec

Title: Perfect score:

US-09-856-070B-29
193
1 BREKEQMMREKEELMLRLQD......EEKTKKAERELSEQIQRALQ 41 Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ezrin [validated]	hypothetical prote	F	ezrin - mouse	r H	in -	¤			trichohyalin - rab	plectin - human	trichohyalin - she	in -	probable seryl-tRN	•	KIAA0642 protein -	translation initia	2	class I INCENP pro	H	l pro	Н	ŭ	hypothetical prote	te	a anti	hypothetical prote	11.4	l prot
SUMMARIES	ΙD	A34400	471	145889	B41129	A41289	539804	539805	A41129	A46127	S28589	G02520	A40691	A45973	B72500	A39638	T00377	T43483	A59404	I50590	I50591	T19756	T15885	E69038	T46368	D96594	92	0	863	145
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	Length	586	630	581	586	577	577	583	583	583	1407	S	1549	œ	463	ဖ	0	1132	œ	839	877	2962	0	174	276	899	743	1164	1378	279
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	Score	191	191	178	173	129	127	121	120	119	79	77	75	73	72	71.5	71	71	71	σ.	69.5	σ,	ø	68.5	ω.	œ	68	68	89	67.5
	Result No.	п	8	m	4	Ŋ	9	7	80	6	10	1 T	12	13	14	15.	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote	hypothetical prote	hypothetical prote	myosin heavy chain	hypothetical prote		Htransporting tw	hypothetical prote	NMD2 protein - yea	microtubule-associ	hypothetical prote	364K Golgi complex	microtubule-associ	hypothetical prote	hypothetical prote	hypothetical prote
T00365	T21379	E70318	833068	T15087	A59287	T07210	F75216	S48244	A54803	T00263	JC5837	T13564	T28184	T00367	T21048
7	~	?	ď	N	7	~	N	N	~	N	~	~	N	N	7
1280	669	400	527	919	1940	175	281	1089	1231	1252	3187	5327	365	756	777
35.0	34.7	34.5	34.5	34.5	34.5	34.2	34.2	34.2	34.2	34.2	34.2	34.2	33.9	33.9	33.9
67.5	67	66.5	66.5	66.5	66.5	99	99	99	99	99	99	99	65.5	65.5	65.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
 ezrin (validated) - human N.altarnata names (vitoxillin, nel nortain, villin o
 C.Species: Homo sapiens (man)
 C;Date: 22-Jun-1990 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
 Kiturunen, O.; Winquist, R.; Pakkanen, R.; Grzeschik, K.H.; Wahlstroem, T.; Vaheri, A. I Biol Peam 264 16737-16737 1000
 A:Title: Cytovilli, a microvillar M-r 75,000 protein. cDNA sequence. prokarvotic express
 A; Reference number: A34400; MUID:89380299; PMID:2674140
 A;Accession: A34400
 A:MOLECULE TYPE: MRNA A:Pesidise: 1-686 FTITE.
A, Cross-references: GB:J05021
1-11 is not given
A.Note: parts of this sequence were confirmed by protein sequencing
 A, GOLILI, A.D.; DITCHOLULE, A.; DSCII, F.S.; MUNICEL, I. EMBO J. 8, 4133-4142. 1989
 A, Title: cDNA cloning and sequencing of the protein-tyrosine kinase substrate, ezrin, rev
A;Accession: S09263
A; Molecule type: mRNA
 A/Residues: 2-586 <gou></gou>
 A):CLOSS-TELEGRODGES: GEI-XXISZLI, NID:GILLSZL; PIDN:CAA5893:1; PID:G31283 D:Banu G. bassmissen H H Van ham bullake M van hamme J Pidning M v Control D C
 i.d 'Tagagar' 'D.'
 A; Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencing
A;Accession: E61002
A; Molecule type: protein
A; Westques: 255-263;194 (2),196-199, X,201;264-270 <bau></bau>
 A;Note: 1t is not cettain whether this material represents ezrin of radixin (see entry A: A:Note: this material corresponds to transformed anithelial amino rell (2001) database or
 C; Comment: This protein is located in microvilli and is proposed to play a role in module
C;Genetics:
A;Gene: GDB:VIL2
A;Cross-references: GDB:120489; OMIM:123900
A) Map position: 6q25-6q25-6d2-6d26 (
 C. Cogetteminty. Cartan, tacintal taminty, process a memorate Justice Justice of Keywords. C. Keywords a artin hinding. Cartackeleton membrane.eeconimted nactein shows the care
 c.ncjmoras actim internal y cycostraterum memarame associated procesu, pinopinopiocesu. F:2-586/product: ezrin #status experimental <mat></mat>
 F;7-291/Domain: protein 4.1 membrane-binding domain homology <b41></b41>
F;553-586/Region: actin binding #status predicted
F:66/Binding site: phosphate (Ser) (covalent) #status predicted F:214.299.332/Binding site: phosphate (Thr) (covalent) #status predicted
4
Query Match 99.0%; Score 191; DB 1; Length 586;
y/.o%; /ative (

Species: Homo sapiens (man)

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A, Molecule type: profein
A, Residues: 53-57,148, L'. 150, 'G'.152-155 < EG3>
A, Molecule transported from NCB backbone (NCBIP:112940)
C, Comment: This protein is located in microvilli and is proposed to play a role in module C, Comment: This protein is located in microvilli and is proposed to play a role in module C, Superfamily: ezrin/radixin/noesin family: protein 4.1 membrane-binding membrane-binding domain homology c, Reywords: actin binding #status predicted AMT>
F, 523-586/Region: actin binding #status predicted
F, 66/Binding site: phosphate (Ger) (covalent) #status predicted
F, 299, 332/Binding site: phosphate (Thr) (covalent) #status predicted
                                                 R. Egerton, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Bretscher, A.; Samelson, L.E. J., Tmmunol. 149, 1847-1852, 1992.
A. Tmmunol. 169, 1847-1852.
A. Title: Identification of earin as an 81-kDa tyrosine-phosphorylated protein in T cells. A. Reference number: A46501; MUID:92388649; PMID:1381389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-577 <LAN>
A;Cross-references: GB:M69066; NID:g188625; PIDN:AAA36322.1; PID:g188626
C;Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma me
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Cross-references: GDB:136819; OMIM:309845
A/Cross-references: GDB:136819; OMIM:309845
A/Map postition: XG11.2-XG412
C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology C;Keywords: actin binding; cytoskeleton; membrane protein
C;Keywords: moesin #status predicted <MATP-
F;2-577/Product: moesin #status predicted <MATP-
F;7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
F;544-577/Region: actin binding #status predicted
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Proc. Natl. Acad. Sci. U.S.A. 88, 8297-8301, 1991
A;Title: Moesin: a member of the procein 4.1-talin-ezrin family of proteins. A;Reference number: A41289; MUID:92020840; PMID:1924289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N/Alternate names: membrane-organizing extension spike protein
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
     A, Cross-references: EMBL:X60671; NID:g50880; PIDN:CAA43086.1; PID:g50881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 27-33, E' <EG2>
A;Residues: 27-33, E' <EG2>
A;Xperimental source: MRL lpr/lpr, T-cells
A;Note: sequence extracted from NCBI backbone (NCBIP:112936)
A;Accession: B46501
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: MRL lpr/lpr, T-cells
A;Note: sequence extracted from NCBI backbone (NCBIP:112938)
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                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: profein
A, Residues: 412-426 < EGE>
A, Experimental source: MRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                A;Accession: C46501
A;Status: preliminary
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R;Lankes, W.T.; Furt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A41289
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 24-Nov-2003
C;Accession: 14588
R;Bergson, C.M.; Zhao, H.; Saijoh, K.; Duman, R.S.; Nestler, E.J.
A;Accession: C:M.; Zhao, H.; Saijoh, K.; Duman, R.S.; Nestler, E.J.
A;Title: Ezrin and osteonectin, two proteins associated with cell shape and growth, are A;Reference number: 145889
A;Accession: 145889
A;Accession: 145889
A;Accession: 145889
A;Accession: Legen, Repainminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: DKF2p762H157.1
C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
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A;Cross-references: GB:N98499; NID:g289407; PIDN:AAA30510.1; PID:g289408
C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
F;7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
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                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 24-Nov-2003 C;Accession: T47177
C;Accession: T47177
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, March 2000
A;Reference number: 224377
A;Accession: T47177
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NiAlternate names: cytovillin; p81 protein; radixin; villin 2

NiAlternate names: cytovillin; p81 protein; radixin; villin 2

Cispecies: Mus musculus (house mouse)

Cipate: 03-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003

Cipate: 03-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003

Cipate: 03-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003

Cipate: 03-Aug-1992 #sequence_revision; B4501; S24200

N. Teukita, S. Tsukita, S.

A. Tsukita, S.

A
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A;Molecule type: mRNA
A;Residues: 1-630 <AAAA>
A;Cross-references: EMBL;AL162086
A;Experimental source: adult melanoma (MeWo cell line); clone DKF2p762H157
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.0%; Score 191; DB 2; Length 63
Best Local Similarity 97.6%; Pred. No. 6.3e-11;
Dest Local Similarity 97.6%; Pred. No. 6.3e-11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
334 EREKEÇUMMEKEKELMLRLÇDYEEKTKKABRELSEÇIQRALQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 EREKEÇMMREKEELMLRLQDYEEKTKKAERELSEQIQRALQ 418
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                                                                                                                                                                                                                                                                                                                 hypothetical protein DKFZp762H157.1 - human (fragment)
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92.2%; Score 178; DB 2; 87.8%; Pred. No. 9.8e-10; 4; Mismatches

Best Local Similarity 87.8 Matches 36; Conservative

à g

Query Match

A)Residues: 1-586 <FUN>

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C;Species: Homo sapiens (man)
C;Date: 2.1-Sep-1993 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C;Accession: A46127
R;Wilgenbus, K.K.; Milatovich, A.; Francke, U.; Furthmayr, H.
R;Wilgenbus, E.K.; Milatovich, A.; Francke, U.; Furthmayr, H.
A;Title: Molecular cloning, cDNA sequence, and chromosomal assignment of the human radixi
A;Reference number: A46127; MUID:93252378; PMID:8486357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1407 <PIE>
A;Residues: 1-1407 <PIE>
A;Cross-references: EMBL:Z19092; NID:g1746; PIDN:CAA79519.1; PID:g1747
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she Covalent modifications to this protein include conversion of arginine to citrulline and t
                                                                               A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-583 «FUNA
A,Note: part of this sequence was confirmed by protein sequencing
A,Note: part of this sequence was confirmed by protein sequencing
C,Comman: Radixin is a capping protein for the barbed end of actin filaments and it is I
C,Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
C,Reywords: actin binding; cyroskeleton
F,77-291/Domain: protein 4.1 membrane-binding domain homology «B41>
F,70-477/Region: prolline-rich
F,550-583/Region: actin binding #status predicted
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S.Superfamily: estin/raddxin/moesin family; protein 4.1 membrane-binding domain homology
C;Keywords: actin binding; cytoskeleton
F;7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
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A,Note: sequence extracted from NCBI backbone (NCBIN:131481, NCBIP:131482)
C,Comment: Radixin is a capping protein for the barbed end of actin filaments and it
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C;Species: Orycrolagus cuniculus (domestic rabbit)
C;Decies: Orycrolagus cuniculus (domestic rabbit)
C;Decession: 528589
R;Fietz, M.J.; Rogers, G.E.
submitted to the EMBL Data Library, December 1992
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A,Accession: $28589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 EKEKERIEREKEELMERLRQIEBOTVKAQKELEEGTRKALE 374
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A; Reference number: A41129; MUID: 92064635; PMID: 1955455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.2%; Score 120; DB 1; 58.5%; Pred. No. 0.00029;
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F;550-583/Region: actin binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
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A; Residues: 1-583 <WIL>
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                                                      A; Accession: A41129
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                                                                                                             RESULT 6
S19804
modelin - pig
my service names: membrane-organizing extension spike protein
C;Species: Sus scrofa domestic pig)
C;Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C;Accession: S13804
C;Accession: Accession: Accession to the plasma
C;Accession: Accession to the plas
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radixin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C;Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C;Date: 19-May-1996
R;Lankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.
Biochim. Biophys. Acra 1216, 470-482, 1993
A;Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification of A;Reference number: 839804; MUD:94092743; PMID:8268231
A;Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification of A;Accession: 839804; MUD:94092743; PMID:916428231
A;Recession: S39804; MUD:94092743; PMID:91642828]
A;Recession: S39805
A;Rocession: S39806
A;Rocession: Sapenday
A;Coss-references: GB:M86444; EMBL:M86391; NID:9164585; PIDN:AAB02865.1; PID:9164586
C;Comment: Radixin is a capping protein for the barbed end of actin filaments and it is C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology cSylomain: protein 4.1 membrane-binding domain homology 
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radixin - mouse
radixin - mouse
radixin - mouse
radixin - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: A41129; S24201
C.Accession: A41129; S24201
C.Accession: A41129; A24201
C.Accession: A37001
C.Core Biol. 115, 1039-1048; 1991
A;Title: Radixin is a novel member of the band 4.1 family.
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65.0%; Pred. No. 6.3e-05;
ive 8; Mismatches 6; Indels
334 EKEKEKIEREKEELMERLKQIBEQIKKAQQELEEQTRRALE 374
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26; Conservative
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Matches 2
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homology <EF2>

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A,Molecule type: DNA
A,Residues: 1.1898 «LEE>
A,Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A,Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A,Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she
C;Genetics: modifications to this protein include conversion of arginine to citrulline and t
A;Gene: GDB:THH
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C;Species: Aeropyrum pernix.
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B72500
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha, A., Hakamaya, M.; Msuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jamazaki, J.; Ko DNA, Res. 6, 83-10, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72500
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A45973
K;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, P.M.
J. Biol. Chem. 268, 12164-12176, 1993
A;Title: The structure of human trichohyalin. Potential multiple roles as a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-463 <KAW>
A; Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA80986.1; PID:g5105674
                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Homo sapiens (man)
C,Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
                                                                                                                                                                Gaps
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C,Superfamily: trifohoyalin; calmodulin repeat homology
C,Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F,49-81/Domain: calmodulin repeat homology <EF2>
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                                                                                                        Query Match 38.9%; Score 75; DB 1; Length 1549; Best Local Similarity 40.5%; Pred. No. 13; Matches 17; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 37.8%; Score 73; DB 1; Length 1898; Local Similarity 41.2%; Pred. No. 24; les 14; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                   3 EKEÇMMREKEELMLRLÇD-----XEEKTKKAERELSEÇIÇR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed (cross-linking) protein.
A;Reference number: A45973; MUID:93280194; PMID:7685034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.3%; Score 72; DB 2;
Best Local Similarity 41.2%; Pred. No. 7.8;
Matches 14; Conservative 8; Mismatches 12
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  F,49-81/Domain: calmodulin repeat home
F,387-851/Region: 28-residue repeats
F,886-1519/Region: 23-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   serine-tRNA ligase
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C;Genteics:
A;Gene: ABE1976
C;Superfamily: serine-tRNA ligas
                                                                                                                                                                                                                                                                                                                                                                                                          trichohyalin - human
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Matches
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C;Genetics:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: G02520
R;McLean, W.H.I.; Smith, F.J.D.
Submitted to the EMBL Data Library, March 1996
A;Reference number: H01385
A;Reference number: H01385
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4574 cMCL>
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C;Genetics:
A;Introns: 46/3
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Superfamily: trichohyalin; calmodulin repeat hand; hair; tandem repeat
F;49-81/Domain: calmodulin repeat homology <EF2>
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C,Superfamily: trichohyalin; calmodulin repeat homology
C,Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
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                                                                                                                                                           40.9%; Score 79; DB 1; Length 1407; ilarity 44.1%; Pred. No. 4.9; Conservative 10; Mismatches 9; Indels
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Best Local Similarity
Matches 15; Conserv
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C;Superfamily:
F;68-283/Domair
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RESULT 12 A40691

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plectin - rat
C:Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A39638; S21876
R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratowa J. Cell Biol. 114, 83-99, 1991
A;Ttle: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with A;Reference number: A39638
A;Ttle: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with A;Reference number: A39638
A;Ttle: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with A;Residues: 1-4687
A;Nolecule type: mRNA
A;Residues: 1-4687
A;Cross-references: EMBL:X59601; NID:g1292885; PIDN:CAA42169.1; PID:g1561642
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; riboscomal protein S;C;Reyworld: cytoskeleton; transmembrane protein
F;6-103/Domain: riboscomal protein S10 homology <RS10>
F;184-399/Domain: alpha-actinin actin-binding domain homology cACT>
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37.0%; Score 71.5; DB 1; Length 4687;

Best Local Similarity 31.8%; Pred. No. 78;

Matches 14; Conservative 15; Mismatches 12; Indels 3;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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EZRI_BOVIN
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drosophila	homo sapien	homo sapien	homo sapien	homo sapien	mus musculu	drosophila	saccharomyc	nicotiana t	schizosacch	homo sapien	methanococc
Q88x83	6dd960	075154	Q9nri5	7spn60	OBMEO	P33438	P53935	Q40554	D09863	Q8nf91	Q58394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
                                                                                                                   Egerton M., Moritz R.L., Druker B., Kelso A., Simpson R.J.; "Identification of the 70kD heat shock cognate protein (HSc70) and alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (cytoplasmic side).
-!- TiSSUE SPECIFICITY: Component of the microvilli of intestinal
epithelial cells.
-!- PTM: Phosphorylated by tyrosine-protein kinases.
-!- SIMILARITY: Contains I FERM domain.
                                                                                                                                                                                                                                                                            PHOSPHORYLATION BY PDGFR.
MEDLINE=92406868; PubMed=1382070;
Krieg J., Hunter T.;
"Identification of the two major epidermal growth factor-induced tyrosine phosphorylation sites in the microvillar core protein ezrin.";
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Structural protein; Cytoskeleton; Phosphorylation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92388649; PubMed=1381389;
Egerton M., Burgess W.H., Chen D., Druker B.J., Bretscher A.,
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2A844D140E3B06CC CRC64;
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 1.1e-10;
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EMBL; J05021; AAA61278.1; ALT INIT.
EMBL; AL162086; CAB82418.1; ALT_INIT.
EMBL; EC013903; AAH13903.1; -.
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InterPro: IPR000299; Eard moesin.
InterPro: IPR000399; Exrad moesin.
Pfam; PP00373; Band 41; 1.
Pfam; PP00375; Eard 41; 1.
PRINTS; PR00935; BAND41.
SMART; SM00295; BAND41.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
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                                                                                          MEDLINE=96311348; PubMed=8713105;
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J. Immunol. 149:1847-1852(1992)
                                                              SEQUENCE OF 171-179 AND 342-349
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PDB; INI2; 25-FEB-03.
WMISS-2DPAGE; P15311; HUMAN.
Genew; HGNC:12691; VIL2.
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MOD_RES
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      REAL SECOND DESIGNATION OF SECOND COORD CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-96239137; PubMed-8660651;
Galat A., Gerbod M.C., Bouet F., Riviere S.;
"Proteins and their amino acid compositions: uniqueness, variability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and applications.";
Arch. Biochem. Biophys. 330:229-237(1996).
-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-!- SUBCELLULAR LOCATION: Microvillar peripheral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergson C.M., Zhao H., Saijoh K., Duman R.S., Nestler E.J.;
Bergson C.M., and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus.";
Mol. Cell. Neurosci. 4:64-73(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY).
PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECD663E5C200FAA3 CRC64;
                                                 333 EREKEÇMMREKEELMLRLÇDYEEKTKKAERELSEÇIÇRALÇ 373
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (cytoplasmic side).
-!- PTM: Phosphorylated by tyrosine-protein kinases.
-!- SIMILARITY: Contains 1 FERM domain.
1 EREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structural protein; CyToskeleton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.2%; Score 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M98498; AAA10510.1; -.
PIR; 145889; 145889.
InterPro; IRR00209; Band 4.1.
InterPro; IRR002099; EZ/rad/moesin.
InterPro; IRR008954; Moesin.
Pfam; PP00373; Band 41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.
SMART; SM0295; B41; 1.
PROSITE; PS000660; FERM 1; 1.
PROSITE; PS00061; FERM 2; 1.
PROSITE; PS50057; FERM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68629 MW;
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                                                                                                                                                                                                        STANDARD;
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145
                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
                                                                                                                                                                                                     EZRI BOVIN
P31976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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MOD_RES
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EMBL; X60671; CAA43086.1; -.
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PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
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Q8HZQ5;
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Best Local
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SOLUTION OF THE PROPERTY OF TH
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RC STRAIN=C57BL/G1 TISSUE=Kidney;

RX MEDINE=C57BL/G1 TISSUE=Kidney;

RX MEDINE=C57BL/G1 TISSUE=Kidney;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Sadi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli M., Ranapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Baldarelli M., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanaj A., Kawaji H., Kawasawa Y., Kedzierski R.M., Xing B.L.,

RA Kanaj A., Kaurochkin I. V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Perrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultena R., Takenaka Y., Taylor M.S., Teadale R.D., Tomite M.,

RA Sultena R., Takenaka Y., Taylor M.S., Teadale R.D., Tomite M.,

RA Sultena R., Takenaka Y., Taylor M.S., Teadale R.D., Tomite M.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninot P., Hayersu N.,

RA Shiraki T., Waki K., Kawai J., Alamawa N., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Litch M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Rannishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Havshizahizahi Y., Waterston R., Lander E.S., Rogers J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C5FBL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hisch F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92064635; PubMed=1955455;
Tinnayama N., Nagafuchi A., Sato N., Tsukita S., Tsukita S.;
"Radixin is a novel member of the band 4.1 family.";
J. Cell Biol. 115:1039-1048(1991).
                                                 1; Indels
                                                                                                                                                                               333 EREKEÇMMREKEBLMLRLQDYEEKTRKAEKELSDQIQRALK 373
                                                                                                                                  EREKEGMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                          EZRI MOUSE
P26640; Q80ZTB; Q9DCII;
01-MAY-1992 (Rel. 22, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
"F-war-2004 (Rel. 43, Last annotation update)
         Pred. No. 1.7e-
                                             4;
    87.8%;
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                                                 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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1D EZRI M
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whitling M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-!- SUBCELIULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Component of the microvilli of intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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82.9%; Pred. No. 4.8e-09;
iive 6; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: Phosphorylated by tyrosine-protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toskeleton, Phosphorylation.
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T -> A (IN REF. 1)
Q -> R (IN REF. 2)
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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EMEL; BC048181; AAH48181.2; --
PIR; B41129; B4129; B4129; B4129; B41129
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us-09-856-070b-29.std.rsp

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SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                             Goldenring J.R., Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                      -!- FTM: Phosphorylated by tyrosine-protein kinases (By similarity).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY PDGFR)
(BY SIMILARITY).
PHOSPHORYLATION (BY PDGFR)
(BY SIMILARITY).
810FA26C69D7ED02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Howden P.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 EQEKEQMLREKEELMMRLQDYEQKTKKAEKELSDQIQRALQ 373
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-203 (Rel. 42, Last amontation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural protein, CyToskeleton, Phosphorylation.
INIT MBT 0 0 BY SIMILARITY.
DOMAIN 1 294 FERM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000299; Band 4.1.
Interpro; IPR000798; Bz/rad/moesin.
Pfam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Placenta;
MEDLINE=92020840; PubMed=1924289;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF537266; AAN06818.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
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                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
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P26038;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECURINE-NOD, TISSUE=Thymus;

RA NEADLINE=2534683; PubMed=12466851;

RADLINE=25354683; PubMed=12466851;

RADLINE=25354683; PubMed=12466851;

RADLINE=25354683; PubMed=12466851;

RADLINE=25354683; PubMed=12466851;

RADLINE=25354683; PubMed=12466851;

RADLINE=25354683; PubMed=12466851;

RADLINE=25364683; PubMed=12466851;

RADLINE=254683; PubMed=12466851;

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RADLINE=254683; RADLINE=254683;

RADLINE=254683; RADLINE=254683;

RADLINE=254683; RADLINE=254683;

RADLINE=254683; RADLINE=2546353;

RADLINE=25573; RADLINE=25573; RADLINE=25573;

RADLINE=25573; RADLINE=25573; RADLINE=2553573;

RADLINE=25573; RADLINE=2553573;

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RADLINE=25573;

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RADLINE=25573;

RADLINE=25573;

RADLINE=25573;

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RADLINE=25573;

RADLINE=255
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SEQUENCE FROM N.A.

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STRAIN=FVBLY, Feingold E.A., Grouse L.H., Derge J.G.,

Attausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Attausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Fonsido M.F., Casavant T.L., Scheetz T.E.,

Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McRwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rasak S.A., McRwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RABAS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Atchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rach Wilting M., Madan A., Young A.C., Shevothenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Mitting M., Madan A., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez CDNA sequences:

Referention and initial analysis of more than 15,000 full-length

RT Human and mouse cDNA sequences:

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                   "A gene family consisting of ezrin, radixin and moesin. Its specific localization at actin filament/plasma membrane association sites."; J. Cell Sci. 103:131-143(1992).
                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                  MEDLINE-93055012; PubMed=1429901;
Sato N., Funayama N., Nagafuchi A., Yonemura S., Tsukita S.,
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                     (Mouse)
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                     musculus
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE=94092743; PubMed=8268231; Lankes W.T., Schwartz-Albiez R., Furthmayr H.; Lonkon and sequencing of porcine moesin and radixin cDNA and identification of highly conserved domains."; Biochim. Biophys. Acta 1216:479-482(1993).

-: FURCHION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.

-: SIMILARITY: Contains 1 FERM domain.
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
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                                          Length 576;
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65.0%; Pred. No. 7.3e-05;
tive 8; Mismatches 6; Indels
                                       66.8%; Score 129; DB 1; Length 57 ilarity 63.4%; Pred. No. 4.8e-05; Conservative 9; Mismatches 6; Indels
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                                                                                                                                                                                        333 EKEKEKIEREKEBLMERLKQIEBQTKKAQQELEEQTRRALE 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Moesin (Membrane-organizing extension spike protein)
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INIT MET 0 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                          576 AA
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InterPro; IPR002299; Band 4.1.
InterPro; IPR00798; Ez/rad/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00773; Band 41; 1.
Pfam; PF00769; ERM; 1.
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P26041;
01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-AUG-1992 (Rel. 23, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M86450; AAB02864.1; -.
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SMART; SM02295; B41; 1.
PROSITE, PS00660; PERM_2; 1.
PROSITE; PS00661; FERM_2; 1.
PROSITE; PS50067; FERM_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Conservative
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                    Query Match
Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                 RESULT 6
MOES_PIG
ID _MOES PIG
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STTY SUBSECTION OF SUBSECTION

RESULT 7 MOES_MOUSE

d

Matches

us-09-856-070b-29.std.rsp

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10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SIMILARITY: Contains 1 FERM domain.
 -!- PTM: Phosphorylated.
-!- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                     EMBL; AF004811; AAB61666.1; -.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/rad/moesin.
Pfam; PF00773; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000299; Band 4.1.
Interpro; IPR000798; Ez/rād/moesin.
Interpro; IPR008995; Moesin.
Pfam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ249838; CAB59977.1; -.
                                                                                                                                                                                                                                                                                                                                 Local Similarity 61.0% es 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHICK
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radixin.
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09PU45;
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
RADI CHICK
ID RADI CI
                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
  Db
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20404063; PubMed=10945828;
Theoharides T.C., Wang L., Pang X., Letourneau R., Culm K.E., Basu S., Mang Y., Correia I.;
"Cloning and cellular localization of the rat mast cell 78-kDa protein phosphorylated in response to the mast cell 'stabilizer' cromolyn.";
J. Pharmacol. Exp. Ther. 294:810-821(2000).
-:- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
[4]
SEQUENCE OF 11-576 FROM N.A.
MEDLINE=92243764; PubMed=1573844;
MEDLINE=92243764; PubMed=1573844;
Furthmay H., Lankes W.T., Amieva M.R.;
"Moesin, a new cytoskeletal protein and constituent of filopodia: its role in cellular functions.";
Kidney Int. 41:665-670(1992).
-i- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-i- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EL -> DV (IN REF. 4).
RA -> SP (IN REF. 4).
5E0F455552E9145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 EKEKEKIEREKEELMEKLKOIEEQTKKAQQELEEQTRRALE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EREKEÇMMREKEELMLRLQDXEEKTKKAERELSEÇIÇRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-3003 (Rel. 42, Last annotation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              Structural protein; Cyfoskeleton.
                                                                                                                                                                                                                                                                                           MGD; MGI:97167; Msn.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; E2/rad/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00173; Band_41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                         AK088336; BAC40290.1; -. BC047366; AAH47366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 371 R
576 AA; 67635 MW;
                                                                                                                                                                                                                                             EMBL; S47577; AAA11762.1; -.
                                                                                                                                                                                                                                                                                   EMBL; M86390; AAA39728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
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SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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331
371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10116;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 035763;
                                                                                                                                                                                                                                                         EMBL;
EMBL;
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MOES_RAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILNE=20225478; PubMed=10760599;
Li W., Crouch D.H.;
Cloning and expression profile of chicken radixin.";
Elochim. Biochys. Acta 1491:327-332(2000).
El- FUNCTION: Probably plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 294 FERM.
576 AA; 67607 MW; 59606907B2D89938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 EKEKEKIEREKEELMEKLKQIEEQTKKAQQELEEQTRRALE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EREKEOMMREKEELMIRLODXEEKTKKAERELSEGIORALO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PFUU(09); bmw, PRINTS; PRO0935; BAND41.
PROSITE; PSO0661; FERM 1; 1.
PROSITE; PSO0661; FERM 2; 1.
PROSITE; PSS0057; FERM 3; 1.
Structural protein; Cytoskeleton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.3%; Score 126; DB 1; 61.0%; Pred. No. 9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [0-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 AA
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68549 MW; 59AEA286DCAF7397 CRC64;

583 AA;

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SQ SEQUENCE
                       Query Match
                                             Matches
                                                                                                                            RESULT
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                        P. SEQUENCE FROM N.A.

MEDIJUNE=94092743; PubMed=8268231;

A Lankes W.T., Schwartz-Albiez R., Furthmayr H.;

Lightification of highly conserved Gmains.";

Lightification of highly conserved Gmains of the blocking barbed end of actin filaments to the plasma membrane.

Lightification of Actin filaments to the plasma membrane.

CHIL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE CELLANGERES AND WITCOTT PHASE, RESPECTIVELY.

LINTERPHASE AND WITCOTT PHASE, RESPECTIVELY.

LINTERPHASE AND WITCOTT PHASE, RESPECTIVELY.

LINTERPHASE AND WITCOTT PHASE, RESPECTIVELY.
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structural protein; Cytoskeleton; Actin-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metăzoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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0
                                                                                                                           64.2%; Score 124; DB 1; Length 583; 61.0%; Pred. No. 0.00014; tive 9; Mismatches 7; Indels
                                                                                                                                                                                       1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEOIORALO 41
                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                             583 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FERM.
GLU-RICH.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, S39805; S39805.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; Ez/rad/moesin.
InterPro; IPR008954; Moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M86444; AAB02865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                          Local Similarity 61.0
nes 25; Conservative
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295
522
477
                                                                                                                                                                                                                                                                                                                     Radixin (Moesin B).
                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PHOSPHORYLATION.
STRAIN=BALB/c; TISSUE=Keratinocytes;
MEDINE=39241736; PubMed=8479753;
Fazioli F., Wong W.T., Ullrich S.J., Sakaguchi K., Appella E.,
Di Riore P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92064635; PubMed=1955455;
MEDLINES=92064635; PubMed=1955455;
Radixin is a novel member of the band 4.1 family.";
J. Cell Biol. 115:1039-1048(1991).
     Length 583;
Match 62.7%; Score 121; DB 1; Length 56 Local Similarity 58.5%; Pred. No. 0.00026; les 24; Conservative 10; Mismatches 7; Indels
                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 28-53 AND 263-277
                                                                                                     1 EREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                583 AA
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PIR; A41129; A41129.
PDB; 1GG6; 28-JAN-03.
PDB; 1GC7; 28-JAN-03.
MGD; MGI:97887; Rdx.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000799; EZ/rad/moesin.
Pfam; PP00769; ERM; 1.
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PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
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SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                           __RADI_MOUSE STANDARD
P26043; Q9QW27;
01-MAY-1992 (Rel. 22, C
10-OCT-2003 (Rel. 42, L
10-OCT-2003 (Rel. 42, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                       Radixin (ESP10)
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halyk S.W.,

Whiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Human and mortal analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilgenbus K.K., Milatovich A., Francke U., Furthmayr H.;
"Molecular cloning, cDNA sequence, and chromosomal assignment of the
human radixin gene and two dispersed pseudogenes.";
Genomics 16:199-206(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
-!- PTM: Phosphorylated by tyrosine-protein kinases (By similarity).
-!- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homos sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences ";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Probably plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane.

-!- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURBOW IN THE
                                                                                                                                                                                                                                                                                                                                ·,
                                                                                                                                                                                                                                                                Length 583;
                                                                                                                                                                                                                                    62.2%; Score 120; DB 1; Length 58
58.5%; Pred. No. 0.00032;
... wiematches 7; Indels
                                                                                                                  E -> A (IN REF. 1).
R -> W (IN REF. 1).
QR -> HA (IN REF. 1).
7121231616C27041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            334 EKEKERIEREKEELMERLRQIEEQTVKAQKELEEQTRKALE 374
                                                                                                                                                                                                                                                                                                                                                                                      1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEGIORALO 41
                                                         POLY-PRO.
EK -> VL (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p35241; Q86v61;
01-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
ACOT-2003 (Rel. 42, Last annotation update)
Radixin.
FERM.
GLU-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=93252378; PubMed=8486357;
                                                                                                                                                                                                              68600 MW;
                                                                                                                                                                                                                                                                                                Best Local Similarity 58.5
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
295
522
477
313
514
514
                         311
470
312
419
419
514
575
583 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                              CONFLICT
                                                                                     CONFLICT
                                                                                                                     CONFLICT
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                       Query Match
                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
ADD AC P3524
ADD AC P3524
DT 01-FE DT 01-FE DT 01-FE DT 10-OC DE RACI X OC NOW NOT DE RACI X OC NOT 
SOLUTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fittz M.J. Rogers G.E.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

FUNCTION: Intermediate filament-associated protein that associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent postsynthetic processing during terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the epidermis.
-i- DOWAIN: Consists of nine domains. Domain 1 contains two EF-hand calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBDIT: Homodimer (Probable).
-!- TISSUE SPECIFICITY: Found in the hard keratinizing tissues such as the inner root sheath (IRS) of hair follicles and medulla, and in the filiform papillae of dorsal tongue epithelium (Probable).
-!- DEVELOPMENTAL STAGE: Expressed during late differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0660; FERM_1; 1.
PROSITE; PSO0661; FERM_2; 1.
PROSITE; PSSO057; FERM_3; 1.
Structural protein; CyToskeleton; Actin-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.7%; Score 119; DB 1; Length 58
58.5%; Pred. No. 0.00039;
Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLU-RICH.
POLY-PRO.
K -> E (IN REF. 2).
889687E1D675FFE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EREKEÇMMREKEELMLRLÇDXEEKTKKAERELSEÇIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1407 AA
                                                                                                                                                                                   Genew; HGNC: 9944; RDX...
MIM; 179410; -..
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; E2/rad/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00773; Band 41; 1.
Pfam; PF00773; Band 41; 1.
PRINTS; PR00935; BAN41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
                                                                                                                    EMBL; L02320; AAA36541.1; -.
EMBL; BC047109; AAH47109.1; -.
                                                                                                                                                     PIR; A46127; A46127.
Aarhus/Ghent-2DPAGE; 2501; IEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 328 K
583 AA; 68564 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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522
477
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                      Actin capping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichohyalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRHY RABIT P37709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is forme most regular and may bind KIF directly by ionic interactions. Domains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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STRAIN=Merino-Dorset horn X Border Leicester; TISSUE-Wool follicles;
MEDLINE=90130632; PubMed=2298812;
Fietz M.J., Preeland R.B., Rogers G.E.,;
"The cDNA-deduced amino acid sequence for trichohyalin, a
                                                                                                                                              PTM: Substrate of transglutaminase. Some 200 arginines are probably converted to citrullines by peptidylarginine deimidase. SIMILARITY: In the N-terminal section; belongs to the S-100

        DOMAIN
        1
        91
        S-100 LIKE.

        2
        33
        EF-HAND 1 (LOW AFFINITY) (POTENTIAL).

        CA BIND
        62
        73
        FF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

        SEQUENCE
        1407 Aa, 183781 MW; AB17D2A159F12B7F CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-93260018; PubMed=7684041;
Fietz M.J., McLaughlan C.J., Campbell M.T., Rogers G.E.;
"Analysis of the sheep trichohyalin gene: potential structural and calcium-binding roles of trichohyalin in the hair follicle.";
J. Cell Biol. 121:855-865(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovis aries (Sheep).
Wakaryota; Metazoca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                     SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.9%; Score 79; DB 1; Length 1407; 44.1%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P02633, 41CB.
InterPro; IPR001751; CaBP S100.
InterPro; IPR002048; EF-hand.
Pfam; PF00026; efhand; 1.
Pfam; PF00023; S_100; 1.
Prodom; PP001407; CaBP S100; 1.
PROSITE; PS001303; SIG CABP; 1.
Reatinization; Calcium-binding; Repeat; Citrullination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1005 REBEQLLQEREEERLRRQERDRKFREEERQLRRQ 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 REKEGMMREKEELMLRLQDXEEKTKKAERELSEG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Trichohyalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z19092; CAA79519.1; -. PIR; S28589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                            different species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P22793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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               Journal of the call envelope to the call envelope or even and and call envelope or even and an another arguments. The call biol intermediate filament associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipoptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent postsynthetic processing during terminal
                                                                                                                                                                                                                                                                                                                                                                           Isold=P22793-2; Sequence=VSP 000847, VSP 000848;
ISOUE SPECIFICITY: Found in the hard keratinizing tissues such as the inner root sheath (IRS) of hair follicles and medulla, and in the prithelia of the tongue, hoof and tunen.

DOWAIN: Consists of nine domains. Domain I contains two EF-hand calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domain 6 is Domains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among
differentiation marker in the hair follicle, contains a 23 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probably converted to cirullines by peptidylarginine deimidase. SIMILARITY: In the N-terminal section; belongs to the S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
EP-HAND 2 (HIGH AFFINITY) (POTENTIAL).
14 X 28 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               different species.
PTM: Substrate of transglutaminase, Some 200 arginines are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z18361; CAA70165.1; -.

R PIE, X51695; CAA35992.1; -.

R PIS, A40691, A40691.

R INSP; P02633, 11G2.

R INTERPRO; IPRO01751; CaBP_S100.

R INTERPRO; IPRO02048; EF-hand.

R Pfam, PP010034; efhand.

R Pfam, PP01023; S 100; 1.

R PROSITE; PS00018; EF HAND, 1.

R PROSITE; PS00109; SI00 CABP; FALSE NEG.

K Keratinization; Calcium-binding; Repeat; Citrullination;

M Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                        SUBUNIT: Homodimer (Probable).
ALTENATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                            [soId=P22793-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-100 LIKE.
                                                                                                                                                                                                                                                                                                                                                                  Name=Short
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CA_BIND
CA_BIND
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Dermatol. 101:658-718(1993)
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CA_BIND
CA_BIND
DOMAIN
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1-11.
1-12.
1-13.
1-14.
23 X 23 AA APPROXIMATE TANDEM REPEATS.
2-1.
2-2.
2-3.
                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            "The structure of human trichohyalin. Potential multiple roles as a functional BF-hand-like calcium-binding protein, a cornified cell envelope precursor, and an intermediate filament-associated (cross-
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILIBE 99280194; PubMed=7685034;
Lee S.-C., Kim I.-G., Marekov L.N., O'Keefe E.J., Parry D.A.D.,
Steinert P.M.;
                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION.
MEDLINE=93315897; PubMed=7686953;
O'Keefe B.U., Hamilton B.H., Lee S.-C., Steinert P.M.;
"Trichohyalin: a structural protein of hair, tongue, nail, and epidermis.";
                                                                                                                                                                                                                                          38.9%; Score 75; DB 1; Length 1549; 40.5%; Pred. No. 9.8;
                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                             1399 1399 E -> G (IN REF. 2).
1549 AA; 201173 MW; B72FB9FF1326E54E CRC64;
                                                                                                                                                                                           Missing (in isoform Short). /FTId=VSP 000847. Missing (in isoform Short). /FTId=VSP_000848.
                                                                                                                                                                                                                                                                     3 EKEQMMREKEELMLRLQD-----XEEKTKKAERELSEQIQR 38
                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                    PRT; 1898 AA
                                                                                                                                                                                                                                               40.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope precursor, and an intermedi.
linking) protein.";
J. Biol. Chem. 268:12164-12176(1993)
                                                                                              2-10.
2-11.
2-12.
2-13.
2-14.
2-15.
2-15.
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2-19.
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les 17; Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
 742
771
796
832
832
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985
1021
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1144
1167
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1507
1197
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                                                                                                                                                                                                                                                                                                                                                     Trichohyalin.
THH OR TRHY OR THL.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                            1228
1251
1274
1297
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1440
1462
1485
1145
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                                                                                                                                                                                                                                                                                                                   TRHY HUMAN
Q07283;
                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                    REPEAT
VARSPLIC
                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                           Query Match
                                                                                                                  REPEAT
             REPEAT
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                           DOMAIN
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Matches
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FUNCTION: Intermediate filament associated protein that associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent postsynthetic processing during terminal
                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation.
-!- SUBUNIT: Monomer (Probable).
-!- TISSUE SPECIFICITY: Found in the hard keratinizing tissues such as the inner root sheath (IRS) of hair follicles and medulla, and in the filiform papillae of dorsal tongue epithelium (Probable).
-!- DEVELOPMENTAL STAGE: Expressed during late differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the epidermis.

--- Consists of nine domains. Domain 1 contains two EF-hand calcium-binding domains. Domains 2-4, 6, and 8 are almost calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely alpha-helical. configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical roof stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: Substrate of transglutaminase. Some 200 arginines are probably converted to citrullines by peptidylarginine deimidase.-!- SIMILARITY: In the N-terminal section; belongs to the S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA TANDEM REPEATS OF R-R-E-Q-Q-L
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EF-HAND 1 (LOW AFFINITY) (POTENTIAL).

EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

EX 13 AA TANDEM REPEATS OF

R-R-E-Q-E-E-E-R-R-E-Q-Q-L.
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GG, GG:0005595; F:calcium ion binding; TAS.
GG:GG:0005599; F:calcium ion binding; TAS.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002013; Spectrin.
InterPro; IPR002013; Spectrin.
InterPro; IPR002013; Spectrin.
InterPro; IPR00340; Spectrin.
IPR0SITE; PS000018; IPR HAND; I.
IPR0SITE; PS000018; IPR0SITE; IPR0SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-1 (APPROXIMATE)
1-2 (APPROXIMATE)
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MIM; 190370; -.
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HSSP; P02633; 4ICB.
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                                          923 162 8 X 30 AA TANDEM REPEATS.

923 952 4-1.

953 962 4-2.

983 1012 4-3.

1003 1042 4-4.

1003 1072 4-5.

1103 1162 4-7.

1103 1162 23 X 26 AA APPROXIMATE TANDEM REPEATS.

1 1754 1801 QERDROYR -> REFEGGTG (IN REF. 2).

1 1857 1857 Q -> K (IN REF. 2).

1 1857 1857 Q -> K (IN REF. 2).

1 1860 1880 V -> G (IN REF. 2).

1 1860 1880 W, A74B5947FB562E31D CRC64;
                                                                                                                                                                                                                                                             Gaps
                      2-9.
9 X 28 AA APPROXIMATE TANDEM REPEATS.
8 X 30 AA TANDEM REPEATS.
4-1.
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37.8%; Score 73; DB 1; Length 1898;
Best Local Similarity 41.2%; Pred. No. 18;
Matches 14; Conservative 10; Mismatches 10; Indels
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Q8772 homo sapien
Q8772 homo sapien
Q89944 homo sapien
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Q9pt71 xenopus lae
Q9ujz6 homo sapien
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1 Brekeqmmrekbelmlrlqd......Bektkkaerelseqiqralq 41
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QBCf87 mus musculu QBCf88 mus musculu QBn824 homo sapien Q25777 plasmodium Q26093 drosophila Q940065 tetrahymena Q9400 hlasmodium	Q81dX6 plasmodium Q81dX6 plasmodium Q80d6 mus musculu Q80h68 pisum sativ Q80h781 mus musculu Q81y82 homo sapien Q81520 homo sapien	mus mus Micty oryz oryz	Q7ts17 mus musculu Q90tus mus musculu Q93226 caenorhabdi Q7ywf1 plasmodium Q8nak8 homo sapien Q8ldw7 arabidopsis
Q8CF87 Q8CF88 Q8N824 Q25777 Q960P3 Q9VV00	Q9DK46 Q81DX6 Q81GGD6 Q8H6S8 Q80TV1 Q9NV82 Q8N5A0	Q7Z2Z8 Q7TT13 Q7TT13 Q86HT4 Q96CG5 Q9FP71 Q9NDI0	Q7TSL7 Q80TU6 Q93326 Q7YWF1 Q8NAK8 Q8LDW7
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ALIGNMENTS

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SEQUENCE FROM N.A.

STRAIN=C57BL/64) TISSUE=Urinary bladder;

MEDLINE=22354633; PubMed=12466851;

The FANTOM Consortium,

The FAINTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

the Allysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAS.";

IN NATURE 420:553-573 (2002).

NATURE 420:553-573 (2002).

RICH 198931; Vil2.

RGD; MGI:99931; Vil2.

RGD; GG:0068565 (C:cytcoskeleton; IRA.

RGD; MGI:99931; Vil2.

RDD: PRO00999; EZ/Fad/moesin.

RICHEPPO: IPR000994; Moesin.

RICHEPPO: IPR000994; Moesin.

REPED: RF00373; Band 41; 1.
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                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Last annotation update)
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PROSITE; PS50057; FERM_3; 1.
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Best Local Similarity 82.9
Matches 34; Conservative
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01-MAR-2003 (TrEMBLrel.
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"Specific expression of ezrin, a cytoskeletal-membrane linker protein, in a subset of chick retinoectal and sensory projections.";

Eur. J. Neurosci. 11:545-558(1999).

EMBL; AB019790; BAA75497.1; -.

GO; GO:0005856; C:cytoskeleton; IEA.

InterPro; IPR000299; Eard M.1.

InterPro; IPR000998; Ez/rad/moesin.

InterPro; IPR008954; Moesin.
                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Best Local Similarity 82.9%; Pred. No. 4.6e-10;
Matches 34; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              CSTRAIN=Structure.

A Gunn-Moore F.J., Tait S., Brophy P.J.;

Gunn-Moore F.J., Tait S., Brophy P.J.;

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF450298; AAL4784-1; -

GO; GO:0005856; C:cytoskeleton; IEA.

InterPro; IPR000799; Band 4.1.

InterPro; IPR000799; Band 4.1.

R Pfam; PF00373; Band 41; 1.

R Pfam; PF00373; Band 41; 1.

R PRMINS; PR00355; BANJ 41.

R SMART: SM00295; BA1; 1.

R PROSITE; PS00660; FERM 1; 1.

R PROSITE; PS00661; FERM 2; 1.

R PROSITE; PS00661; FERM 2; 1.

R PROSITE; PS00661; FERM 3; 1.

R PROSITE; PS00661; FERM 3; 1.

R PROSITE; PS00661; FERM 3; 1.
                              169 EREKEÇMLREKEELMIRLQDYEÇKTKRAEKELSEQIEKALQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 EREKEQMLREKEELMLRLQDFEQKTKRAEKELSEQIEKALQ 374
  1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEQIORALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EREKEÇMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                               01-MDR-2002 (TrEMBLrel. 20, Created)
01-MDR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                    455 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=White Leghorn, TISSUE=Brain;
MEDLINE=99171943; PubMed=10051754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                    PRT;
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Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                         Ezrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                              Q8VHK3;
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                                                                                                                                                                    Q8VHK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
Q9YGW6
                                                                                                                  RESULT 2
Q8VHK3
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Brakryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Xenopus laevis (African clawed frog).
Xenopus Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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                                                                                                                                                                               Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC049479; AA449479-11.
R EMBL; BC049479; AA449479-11.
R InterPro; IPR000299; Band 4.1.
R InterPro; IPR000299; Band 4.1.
R Pfam; PF00373; Band 4.1; 1.
R Pfam; PF00373; Band 4.1; 1.
R RPMTS; RR00935; BAN41.
R RPMTS; RR00935; BAN41.
R RPMST; SR00695; BAN1 1.
R RPOSITE; PS00661; FERM 1; 1.
R RROSITE; PS00661; FERM 2; 1.
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PRINTS; PR00935; BAND41.

SMART; SM00295; B41; 1.

PROSITE; PS00660; FERM 1; 1.

PROSITE; PS500661; FERM 2; 1.

SEQUENCE 5850057; FERM 3; 1.

SEQUENCE 585 AA; 69366 MW; 854C6348F783CAEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 439 439 MW; 8C907EB06D0A3D12 CRC64;
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                                                                                                                                                                                                                                                                                                             334 EREKEÇMLREKEELLVRLQEYEVKTKRAEKELSDQIQRALQ 374
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                                                                                                                                                                                                                                                                              1 EREKEOMMREKEELMLRLQDXEEKTKKAERELSEQIORALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                             83.9%; Score 162; DB 13; 78.0%; Pred. No. 7.7e-09; tive 7; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
60.6%; Score 117; DB 13;
Best Local Similarity 56.1%; Pred. No. 0.00024;
Matches 23; Conservative 12; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 AA
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                               Query Match
Best Local Similarity 78.05
Matches 32; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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A Chen Z.C., Fadiel A., Naftolin F.;
Chen Z.C., Fadiel A., Naftolin F.;
"Mutation of ezrin gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
R GO, GO:000586; C.Y.Coskeleton; IEA.
R GO, GO:00586; A.Y.Coskeleton; IEA.
R InterPro; IPR000799; Band 4.1.
R InterPro; IPR000799; EZ/rad/moesin.
PROSITE; PSSO057; PERM; 1.
                                                                                                                                                                                                                                                                                                                           Query Match 52.8%; Score 102; DB 4; Length 158; Best Local Similarity 95.5%; Pred. No. 0.0033; Matches 21; Conservative 0; Mismatches 1; Indels
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              TISSUE=Ovary;
Chen Z.C., Fadiel A., Naftolin F.;
Chen Z.C., Fadiel A., Naftolin F.;
Ezrin gene mutation in ovarian cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF188897; AAF03155.1; -
GO; GO:000585; C:ytoskeleton; IEA.
GO; GO:000585; E.c.ytoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/rad/moesin.
PROSIN: PROSIN: 1.
PROSIN: FERM; 1.
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158 AA; 19086 MW; 86E92E1BC6F2957E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment).
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-UTN-2003 (TrEMBLrel. 24, Last ann
Ezrin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 EREKEÇMMREKEELMLRLODYE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              1 EREKEOMMREKEELMLRLODXE 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EREKEOMMREKEELMLRLO 19
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SEQUENCE FROM N.A.
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SEQUENCE
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Best Local &
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Q9UJZ8;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 53.9%; Score 104; DB 4; Length 159; Local Similarity 91.3%; Pred. No. 0.0021; es 21; Conservative 1; Mismatches 1; Indels
Armstrong N.A., Thorn J.M., Kay B.;
Submitted (JUN.1995) to the EMBL/GenBank/DDBJ databases.
BMBL; U29763; AAR721215.1, -.
GO; GO:0005856; C:cytoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/rad/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00773; Band 41; 1.
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Fadiel A., Chen Z.C., Naftolin F.;
"Mutation of ezini gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF189213; AAF03156.1; --
GO; GO:0005865; G:cytoskeleton; IEA.
InterPro; IPR000799; Band 4.1.
InterPro; IPR000799; Ez/rād/moesin.
PROSITE; PS50057; FERM, 1.
                                                                                                                                                                                                  PRINTS; PR00935; BAND41.
SWART; SW00295; B41; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
SEQUENCE 580 AA; 68134 MW; 1006A7E9E5887074 CRC64;
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159 AA; 19234 MW; 7C39838BF7BA70FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EREKEOMMREKEELMIRLODXEEKTKKAERELSEOIORALO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 EREKEQMMREKEELMLRLQDYED 159
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Q9UJZ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UJZ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UJZ7
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Matches
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299032
AC 29903
AC 29903
DT 01-M
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Jonca J., Allaman J.M., Radigruber G., Meda P., Kiss J.Z., French L.E., Masson D.; French distribution of murine 115-kDa epithelial microtubule-associated protein (B-MAP-115) during embryogenesis and in adult organs suggests a role in epithelial polarization and differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.1%; Score 87; DB 4; Length 152; 100.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen Z.C., Fadiel A., Naftolin F.;

"Mutation of cytovillin gene in glioblastoma.";

Submitted (SEP-199) to the EMBL/GenBank/DDBJ databases.

EMBL, AF1900559, AAF03158.1;

GO, GO:0005856, C:cytoskeleton; IEA.

InterPro; IPR000299; Band 4.1.

InterPro; IPR000789; Ez/rād/moesin.

PROSITE; PS50057; FERM_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
Indels
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152 AA; 18416 MW; B7FCE817DD2B9291 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                   152 AA
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  7; Mismatches
                                                   1 EREKEOMMREKEELMIRLODXBEKTKKAER 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microtubule-associated protein, MAP-115.
MTAP7 OR MAP.
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98418230; PubMed=9745708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pre
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                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 18; Conservative
  18; Conservative
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                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Cytovillin 2 (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=B6CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                               Q9UJZ2;
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Q9UJZ2
     Matches
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Strausberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

R. Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

Altschul S.F.; Jordan H., Moore T., Max S.I.; Wang J., Hsich F.,

R. Diatchenko, L.; Marusina K.F.; Farmer A.A.; Rubin G.M.; Hong L.;

R. Diatchenko, L.; Modin T.B.; Toshiyuki S., Carninoi P., Prange C.;

Raha S.A.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Rosak S.A.; Modenn P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

Richards S.A.; Modenn P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

Richards S.A.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

Richards S.A.; Modenn P.M.; Sodergeen E.J.; Lu X.; Gibbs R.A.;

Richards S., Worley D.M.; Sodergeen E.J.; Lu X.; Gibbs R.A.;

Raha S.S.; Worley N.M.; Sodergeen E.J.; Lu X.; Gibbs R.A.;

Raha S.B.; Morley M.S.; Shevchenko Y.; Skalska U.; Smallus D.E.; Schnerch A.; Schein J.E.;

Rayayusha M. I.; Skalska U.; Smallus D.E.; Schnerch A.; Schein J.E.;

Rayayusha M. Madan A.; Yough M.S.;

Rayayusha M. M.; Shalska U.; Smallus D.E.; Schnerch A.; Schein J.E.;

Rayayusha M. M.; Shalska U.; Smallus D.E.; Schnerch A.; Schein J.E.;

Rayayusha M. M.; Shalska U.; Smallus D.G.; Schnerch A.; Schein J.E.;

Rayayusha M. M.; Shalska U.; Smallus D.G.; Schnerch A.; Schein J.E.;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·,
                                                        TISSUE-Placenta;
A Chen Z.C., Fadiel, A, Naftolin F.;
C. Mutation analysis of ezrin gene in cancer cells.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RMBL; AF187552; AAD56713.1; -.
GO, GO:0005865; C:Cytoskeleton; IEA.
InterPro; IPR000799; Ez/rad/moesin.
R Therepro; IPR000799; Ez/rad/moesin.
Pfam; PF00779; BRM, 1.
RPOSITE; PS50057; FRRM, 1.
RPOSITE; PS50057; FRRM, 1.
RON_TER 161 161
NON_TER 161 161
SEQÜENCE 161 AA; 19439 MW; SFD6EB910E017099 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 4; Length 161;
Pred. No. 0.035;
0; Mismatches 0; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053417; AAH53417.1; -.
Hypothetical protein.
SEQUENCE 389 AA; 46367 MW; 6EAZEDCBA9BB5A76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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60.0%; Pred. No. 0.16;
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100.0%; Pred. No. v..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 EREKEÇMMREKEELMLRLÇ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EREKEQMMREKEELMLRLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 100.0
Watches 19, Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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01-OCT-2003 (
01-OCT-2003 (
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Kawakani B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sato H., Wakhawa T., Kimura K., Yamashita H., Matsuo K., Nakamia Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma P., Sekine M., Kikuchi H., Kanda K., Wagatsuma P., Masuo K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y., Supan S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, AKO97517, BACC0504-1; -

IntherPro, IPR000533, Tropomyosin.
                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.6%; Score 74.5; DB 4; Length 621; 35.3%; Pred. No. 7.5; tive 11; Mismatches 11; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621 AA; 77106 MW; 67938434F3BE7929 CRC64;
                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ40198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 35.3%
tes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
                                                                                                                                                                                              (Human)
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                    rissum=Testis;
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Q8N9W4;
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   A RAP RAP REPERENT RE
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                 Score 75; DB 11; Length 730;
Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.9%; Score 75; DB 11; Length 738; 48.6%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
(DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                           EMBL, Y15197, CAA75495.1; -.
EMBL, AB098611; BAC53729.1; -.
MGD, MGI:1328328; Mrap7.
InterPro, IPRO08604; E-MAP-115.
Pfam; PF0672; E-MAP-115; I.
SEQUENCE 730 AA; 82021 MW; F44B4201DB8F5A17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC052637; AAH52637.1; -.
SEQUENCE 738 AA; 82839 MW; BFA2DIEICC78815F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to microtubule-associated protein 7.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 REKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 REKEÇMMREKEELMLRLQDXEEKTKKAERELSEQIQR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738 AA.
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                                                                                                                                                                                                                                                                                                 38.9%;
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.5.
Best Local 8. Conservative
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es 18; Conservative
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SEQUENCE FROM N.A.
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Submitted
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Matches
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Q7TQL9
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Q8N7Z2
ID Q8N7Z
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Gaps

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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Ishidashi T., Kanehori K., Takiguchi S., Kusano J., Watanabe M., Hiraoka S., Murakawa K., Takiguchi S., Yamashita H., Chiba Y., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawal-Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Pulii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK093463; BAC04173.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPRO00533; Tropomyosin.
PRINTS; PRO0194; TROPOMYOSIN.
Hypothetical protein.
SEQUENCE 650 AA; 79069 MW; 2DCE6078E002D031 CRC64;
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                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.1%; Score 73.5; DB 4; 42.5%; Pred. No. 9.9; tive 9; Mismatches 11;
                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein FLJ36144.
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Best Local Similarity 42.59
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Search completed: August 16, 2004, 09:45:40 Job time: 78 secs

us-09-856-070b-29.std.rspt

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

August 16, 2004, 09:50:52; Search time 55 Seconds (without alignments) 210.626 Million cell updates/sec Run on:

US-09-856-070B-29 Title: Perfect score:

41

1 EREKEQMMREKEELMLRLQD......EEKTKKAERELSEQIQRALQ OLIGO Gapop 60.0 , Gapext 60.0 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

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9586 Total number of hits satisfying chosen parameters: Word size :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_29Jan04:* 1: genesem1100 geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* 2 6 4 5 9 7 8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

	Description	Aab82020 Human hep	Aag73954 Human col	Adc31630 Human nov	Human	Aay27443 Amino aci	Human :	Aau30004 Novel hum	1 Human	6 Human	Aab82035 Human hep	0 Novel	Aab82037 Human hep	Aab82038 Human hep	Aau68025 Human Bre	9 Human	Aab07823 Amino aci	σ.	Abm69116 Photorhab	Add22984 Human pro		Abg16577 Novel hum	Abol5000 Human NOV	Abol5001 Human NOV	Abg61631 Streptoco	-
SUMMARIES	DB ID	4 AAB82020	4 AAG73954	7 ADC31630	7 ADE63987	2 AAY27443	7 ADC31629	4 AAU30004	7 ADC31631	3 AAB53356	4 AAB82035	4 AAU33060	4 AAB82037	4 AAB82038	4 AAU68025	4 AAB82039	3 AAB07823	4 AAB82019	6 ABM69116	7 ADD22984	4 AAU00244	4 ABG16577	6 ABO15000	6 AB015001	5 ABG61631	7 ADE54611
	Length DB	34	436	579	585	586	611	622	628		14		-	П			m	32	7	٣	363	ß	ß	555	563	576
d	Query Match	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	œ	34.1	29.3	24.4	22.0	19.5	19.5	19.5	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1
	Score	20	20	20	20	20	20	20	20	20	14	12	10	9	æ	æ	œ	7	7	7	7	7	7	7	7	7
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ADD45108	ABR59727	ADB70362	ADC77532	ABU89709	ADB79911	ADC56738	ABG19947	AAW22780	AAW71293	ADB65482	AAY53008	AAE01020	AAB24238	AAB93007	AAB95640	AAE22856	AAU99661	ADC21697	ADD14124
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576	577	577	577	583	583	583	593	645	645	650	667	689	742	796	817	1215	21	1215	1272
17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1
7	1	7	7	7	٢	1	7	7	7	7	7	7	7	7	7	7	-	7	1
26	27		6 0			32	. E	34	35	36	37	38	39	40	41	42	4 ,	4	45

ALIGNMENTS

AAB82020 standard; peptide; 34 AA. Human hepreceptor domain B. (first entry) 13-JUN-2001 AAB82020;

Human; hepreceptor domain B; cytostatic; anti-HIV; antibiotic; nootropic; immune response inducer; ezrin; infectious diseases; cancer; HIV-related dementia.

Homo sapiens

/note= "Optionally phosphorylated" Location/Qualifiers Key Modified-site

GB2354241-A.

21-MAR-2001.

99GB-00021881. 99GB-00021881 17-SEP-1999; .7-SEP-1999;

я О (HOLM/) HOLMS

Holms RD;

WPI; 2001-293287/31.

Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating infectious diseases and cancer.

Claim 5; Page 36; 42pp; English.

The present sequence is domain B of human hepreceptor of human ezrin. The hepreceptor is a novel active site in human ezrin. Bzrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AAB82041) that bind to hepreceptor with greater affinity than HBPL (see AAB82046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present sequence assembles into two anti-parallel

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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased that effect the activity of P by expression in a patient's genome that effect the activity of P by expression is patient's genome to produce the colon cancer-associated Ps. Ps y inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinoms and cancers. AAH37196 to AAH37204 and AAH37789 represent

2 sequences used in the exemplification of the present invention. N.B.

2 pages 666 to 682 and page 7053 of the sequence listing were missing at the others.

2 time of publication, meaning no sequences are present for SEQ ID NO:1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                           Length 34;
                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen protein SEQ ID NO:4718.
                                                                         Score 20; DB 4; Le
Pred. No. 1.9e-12;
0; Mismatches 0;
helices with hepreceptor domain A (see AAB82019)
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                                                                                                                                                                                                                                                                                        AAG73954 standard; protein; 436 AA
                                                                                                                                                      22 EEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                        15 EEKTKKAERELSEQIQRALQ 34
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                                                                         Query Match
Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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Best Local Similarity 100.8
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              colorectal carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAH33385
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                                        Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                   03-SEP-2001
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                                                                                                                                                                                                                                                                                                                              AAG73954;
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                                                                                                                                                                                                                                                   RESULT 2
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The invention relates to 971 novel human cDNA sequences (ADC29919-CC ADC30890-ADC31860). The invention also relates to notice acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a mucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody companies or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of polypeptide of the invention. The invention further discloses methods of polypeptide of the invention. The invention methods for the identification of compounds that modulate the companies of monoclonal antibodies for carrying out the methods of the invention of conting sequences corresponding to the cDNA sequences of the invention or expression or activity of the polymuclectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are corresponding to the cDNA sequences of the invention are contiguated of multiple and polypeptides of the invention are contiguated of multiple and configurations responsible for garetic disorders or other configurations responsible for garetic disorders or other craits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynuclectide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                    ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q25.2-26.
                                                                                                                                                                                                                                                                                                                                    Human, diagnostic; drug screening; forensics; gene mapping;
biodiversity assessment; Parkinson's disease; Alzheimer's disease;
neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weng G;
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Wang D, Ma Y, Asundi V, Wang Z,
                                                                                                                                                                                                                                                                                       Human novel polypeptide sequence, SEQ ID NO:1712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 1712; 1185pp; English.
                                                                                                                                                      ADC31630 standard; protein; 579 AA
                                      184 EREKEÇMMREKEELMLRLQD 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-2002; 2002WO-US030474.
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                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADC30659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                              18-DEC-2003
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                                                                                                                                                                                                     ADC31630;
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             disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The mucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmet directly from WIPO at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                       ó
disease and other neurodegenerative diseases, anaemia, platelet
                                                                                                                                                                                                                                                               / Match 48.8%; Score 20; DB 7; Length 579; Local Similarity 100.0%; Pred. No. 2.2e-11. and 12 of 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein P15311, SEQ ID NO 9933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE63987 standard; protein; 585 AA.
                                                                                                                                                                                                                                                                                                                                                                                         302 BREKEOMMREKBELMLRLOD 321
                                                                                                                                                                                                                                                                                                                                                 1 EREKEOMMREKEELMLRLOD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002; 2002WO-US025765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-268312/26.
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                                                                                                                                                                                                                       Sequence 579 AA;
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         polymprolectides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more pain and a pharmaceutical composition comprising the one or more modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "the Tyr at this position can be mutated (preferably to a Phe) to construct an ezrin mutant of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a pharmaceutical composition containing ezrin protein, RNA or DNA mutated on tyrosine 353, or a functional fragment or derivative of the ezrin mutant. The new composition is useful for prevention and/or treatment of tumors, and especially metastasis. The present sequence represents the amino acid sequence of human ezrin (before the maturation by deletion of the first amino acid Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition for prevention and treatment of tumors and metastasis.
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                                                                                                                                                                                                                                                                                                                       48.8%; Score 20; DB 7; Length 585;
100.0%; Pred. No. 2.3e-11;
live 0; Mismatches 0; Indels
compound that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pharmaceutical; ezrin; mutant; tumor; metastasis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of human ezrin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gautreau A, Louvard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY27443 standard, protein; 586 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  333 EREKEÇMMREKEBLMLRLÓD 352
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100.08; Fre
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CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-561851/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 354
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                        Sequence 585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1999;
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(CNRS )
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useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other trains. For assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelat disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptiace are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence of data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the print of the print

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DB 7; Length 611; 2.3e-11; 0; Indels

100.0%; Prec. ... 48.8%; Score 20; 100.0%; Pred. No.

Query Match
Best Local Similarity 100.0
Matches 20, Conservative

Sequence 611 AA;

1 EREKEQMMREKEELMLRLQD 20

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the indentification of compounds that modulate the invention; methods for the indentification of compounds that modulate the invention; methods for the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32827) and the polypeptides encoded by the contigs (ADC33628 ADC33394). The nucleic acids and polypeptides of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; hoddiversity assessment; parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6g5.2-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J, Wehrman
Wang Z, Weng G;
                                    48.8%; Score 20; DB 2; Length 586; 100.0%; Pred. No. 2.3e-11;
                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Human novel polypeptide sequence, SEQ ID NO:1711.
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Shosh M, Wang D, Ma Y, Asundi V,
ente D, Drmanac RT;
                                                 100.0%; Prec. ...
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                                                                                                                                                                                                                                                           ADC31629 standard; protein; 611 AA
                                                                                                                                                   334 EREKEÇMMREKEELMLRLQD 353
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                                                                                                                       1 EREKEQMMREKEELMLRLQD
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                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                               Conservative
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                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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Sequence 586 AA;
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Zhou P, G
                                                                                                                                                                                                                                                                                                    ADC31629;
                                          Query Match
                                                                               Matches
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The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                               Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration; immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 219; 765pp; English.
                                                                                        AAU30004 standard; protein; 622 AA
                                                                                                                                                                                               Novel human secreted protein #495.
334 EREKEOMMREKEELMIRLOD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT;
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26-JAN-2001; 2001US-00770160.
                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                           WO200179449-A2
                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                               18-DEC-2001
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                                                                      AAU30004
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Wehrman T;

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to mucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody polynucleotides or polypeptides of the invention; and method of detecting polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
             as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; biodiversity disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; antiparemic; anticoagulant; thrombolytic; vulnerary; antitucer; osteopathic; immunosuppressive; antiinfammatory; cytostatic; gene therapy; chromosome 6q2s.2-26.
are useful in genetic vaccination, testing and therapy, and can be used
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                                                                                                                                                                            Length 622;
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Wang Z, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel polypeptide sequence, SEQ ID NO:1713.
                                                                                                                                                                            Score 20; DB 4; Le
Pred. No. 2.4e-11;
0; Mismatches 0;
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Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 1713; 1185pp; English.
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Wang D, Ma Y, A
                                                                                                                                                                                                                                                                                                                                                                             ADC31631 standard; protein; 628 AA
                                                                                                                                                                                                                                                                                      EREKEOMMREKEELMLRLOD 389
                                                                                                                                                                48.8%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                  1 EREKEOMMREKEELMLRLOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                Conservative
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N-PSDB; ADC30660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang J,
                                                                                                                                                                                               Local Similarity
nes 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang TY, Zhang J,
Zhou P, Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                              Sequence 622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003029271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                   ADC31631;
                                                                                                                                                                                                                                                                                        370
                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                  ADC3163
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invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polynuclectide probes and/or monoclonal antibodies for carrying out the methods of the cinvention; methods for the identification of compounds that modulate the expression or activity of the polynuclectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention of (ADC31364). The nucleic acids and polypeptides of the invention are caseful in diagnostics, drug screening, forensics, gene mapping, in the contists, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's concer. The nucleic acids may also besed as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically contained human polypeptide sequence of the invention. Note: The sequence data for this patent did not forme darker by from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; general disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer antigen protein sequence SEQ ID NO:896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 7; Li
Pred. No. 2.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 48.8%; Score 20; DB Similarity 100.0%; Pred. No. 2.4 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB53356 standard; protein; 635 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 EREKEÇMMREKEELMLRLQD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EREKEOMMREKEELMLRLOD 20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 628 AA;
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Gaps

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Length 14;

34.1%; Score 14; DB 4; Length 14; 100.0%; Pred. No. 6.6e-07; tive 0; Mismatches 0; Indels

Conservative

hepreceptor (AAB82019 and AAB82020)

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(HOLM/) HOLMS
                                                                                  Homo sapiens
                                                                                                 17-SEP-1999;
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                                                                   13-JUN-2001
                                                                                     GB2354241-A
                                                                                         21-MAR-2001
                                                               AAB82035;
                                                                                                        Holms RD;
                                       Query Match
                                                        RESULT 10
                                                         AAB8203
8
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AAU33060 standard; protein; 52 AA.
                                                                                                      Local Similarity
les 14; Conserv
                                        Sequence 14 AA;
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Matches
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SXS
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0
                                                                          called human colon cancer antigens, given in AAB52234 to AAB5406. The human colon cancer antigens can have cytostatic, cardioactive, muscular, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, infectious diseases, and cardiovascular disorders, infectious diseases; and cardiovascular disorders infectious diseases; and cardiovascular disorders. AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating infectious diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see ABB2021 to AAB82046) that bind to hepreceptor with greater affinity than HEPI (see AAB82046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present peptide binds to domains A and B of the
                                                             AAC97991 to AAC98763 encode the human colon cancer associated proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; hepreceptor; cytostatic; anti-HIV; antibiotic; nootropic;
immune response inducer; ezrin; infectious diseases; cancer;
HIV-related dementia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%; Score 20; DB 3; Length 635; 100.0%; Pred. No. 2.4e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human hepreceptor domain A/B binding peptide Rupe1024.
               Claim 11; Page 1449-1451; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82035 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 EREKEÇMMREKELMLRLÇD 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EREKEOMMREKEELMLRLQD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
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Matches 20; Conserv
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopolesis; and in bone, cartilage, tendon and/or retreate stem tell almamatory agents; and in treatment of leukaemias. AUC29510-AAU33304 represent the amino acid sequences of novel human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                    Human, vaccination; gene therapy, nutritional supplement,
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 0.00019;
iive 0; Mismatches 0;
                                                                  Novel human secreted protein #3551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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(first entry)
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Best Local Similarity 100.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   WO200179449-A2.
                                                                                                                                                                                                                                                                                                Homo sapiens.
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The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AAB82021 to AAB82041) that bind to hepreceptor with greater affinity than HEP1 (see immune response, and for binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present peptide binds to domain A of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Breast cancer-associated protein isoform, BPI-1 peptide #3.
                            Human, hepreceptor; cytostatic; anti-HIV; antibiotic; nootropic;
immune_response inducer; ezrin; infectious diseases; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Breast cancer-associated protein isoform; breast cancer; immunogen; cytostatic; BPI; tryptic digest peptide.
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No. 0.046;
0; Indels
Human hepreceptor domain A binding peptide Rupe2132.
                                                                                                                                                           /note= "Optionally phosphorylated"
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100.0%; Pred. No. 0.0
iive 0; Mismatches
                                                                                                                             Location/Qualifiers
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9; Conservative
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                                                                HIV-related dementia.
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                                                                                                                                                                                                                                                                                                                       (HOLM/) HOLMS R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 AA;
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                                                                                                                             Key
Modified-site
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                                                                                                  Homo sapiens
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating infectious diseases and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AABS2021 to AABS2041) that bind to hepreceptor with greater affinity than HEPI (see AABS2046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present peptide binds to domain A of the hepreceptor (AABS2019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                         Human; hepreceptor; cytostatic; anti-HIV; antibictic; nootropic; immune response inducer; ezrin; infectious diseases; cancer; HIV-related dementia.
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                                                                                                                                                                                                              Human hepreceptor domain A binding peptide Rupe2032
                                                                                                                                                                                                                                                                                                                                                             11
/note= "Optionally phosphorylated"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                    AAB82037 standard; peptide; 13
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                                                                                                                                                                                                                                                                                                                Homo sapiens
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AC AAB8
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DT 13-5
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The invention relates to diagnosing, determining the stage or severity, or identifying the risk of a subject developing cancer (especially breast cancer), or monitoring the effect of therapy on a subject with cancer, comprising analysing a test sample using two-dimensional electrophoresis and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The methods disclosed are used for the diagnosis and prognosis of breast cancer, for determining the severity of breast cancer, and monitoring the effect of therapy administered to a subject. Antibodies raised against the binding domain of a BPI, the binding the function of a BPI cast cancer. The methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the compositions are more potent, specific, and has a more rapid effect with fewer side effects that other prior art methods. The present sequence is a tryptic digest peptide from a BPI of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                      ōţ
                                                                                                                                                  Identifying proteins for clinical screening, diagnosis and prognosis breast cancer, comprises detecting Breast Cancer-Associated Protein Isoforms (BPIs) using two-dimensional electrophoresis.
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immune response inducer; ezrin; infectious diseases; cancer;
HIV-related dementia.
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                                                                                  Waterfield MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human hepreceptor domain A binding peptide Rupe2232.
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                                                                                  Parekh RB,
                                                  (OXFO-) OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                    Page MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB82039 standard; peptide; 11 AA
                                                                                                                                                                                                                      Claim 9; Page 43; 197pp; English
20-MAR-2000; 2000GB-00006695.
24-MAR-2000; 2000GB-00007265.
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Matches 8; Conservative
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Holms RD;

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Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating infectious PT diseases and cancer.

XX

Aiseases and cancer.

XX

Claim 26, Page 37; 42pp; English.

XX

Claim 26, Page 37; 42pp; English.

XX

Che structure of the cortical cytoskeleton to control cell surface company. The present invention relates to peptides (see AAB82021 to CAAB82041) that bind to hepreceptor with greater affinity than HEP1 (see CC topography. The present invention relates to peptides are useful for inducing CC immune response, and for treating infectious diseases, cancer and HIV-CC AAB82046). The hepreceptor binding peptides are useful for inducing CC immune response, and for treating infectious diseases, cancer and HIV-CC related dementia. The present peptide binds to domain A of the Best Local Similarity 100.0%; Pred. No. 0.41; Length 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ABELDALELOD 8

Search completed: August 16, 2004, 09:54:33

Job time : 56 secs
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RESULT 2
US-09-040-725A-2
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Sequence 11628, A
Sequence 26, Appl
Sequence 26, Appl
Sequence 379, App
Sequence 7013, App
Sequence 7, Appl
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Sequence 2, Appli
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Sequence 7, Appli
Sequence 5, Appli
Sequence 6304, Ap
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                                                                                                                                        August 16, 2004, 09:54:23 ; Search time 39 Seconds (without alignments) 54.273 Million cell updates/sec
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1 EREKEQMMREKEELMLRLQD......BEKTKKAERELSEQIQRALQ
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1. /ogn2 6/ptodata/2/iaa/5A_COMB.pep:*

1. /ogn2 6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*

4: /ogn2 6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6:
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-040-725A-2
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US-08-687-080-47
US-09-168-595-144
US-09-108-595-144
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US-09-134-000C-6304
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Sequence 2, Application US/09040725A; Sequence 2, Application US/09040725A; Batent No. 6399584; Batent Care No. 6399584; Batent No. 6399584; Baten
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APPLICANT: Institut Curie
APPLICANT: CRS
APPLICANT: Arpin, Monique
APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
APPLICANT: Carpardi, Alexis
APPLICANT: Couvard, Damiel
TITLE OF INVENTION: Parmaceutical composition containing ezrin mutated
TITLE OF INVENTION: On tyrosine 353
FILE REPRENCE: 391082000100
CURRENT FILING DATE: 1998-03-18
NUMBER OF SED ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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TYPE: PRT
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US-09-134-001C-3736

US-08-960-780-23

US-09-073-898-23

US-09-073-898-23

US-09-850-351A-23

US-09-850-351A-29

US-09-850-351A-29

US-09-872-8-27-8

US-09-54-552-8

US-09-54-552-8

US-09-511-8338-14

US-09-971-8238-14

US-09-017-8238-14

US-09-017-8238-14

US-09-017-8238-14

US-09-017-8238-14

US-09-017-8238-14

US-09-11-393-3

US-09-11-393-13

US-08-11-939-13
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               Query Match
Best Local Similarity
Matches 20; Conserval
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TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
FILE REFERENCE: CSHL90-04FZA
CURRENT APPLICATION NUMBER: 103/09/848,294
CURRENT PILING DATE: 290-01-05-03
PRIOR APPLICATION NUMBER: 09/725,251
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR FILING DATE: 1995-01-04
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR PILING DATE: 1991-03-01
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
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| Patent No. 5821091
| Canada Linponana Linguist Control of Canada Linguist Caracata Linguist Lingui
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.1%; Score 7; DB 4;
100.0%; Pred. No. 14;
tive 0; Mismatches
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NAME: Sholtz, Charles K.
RESERGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                   RESULT 5
US-09-848-294-5
Sequence 5, Application US/09848294
Patent No. 6479640
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0
Matches 7; Conservative
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRGANISM: Homosapiens US-09-848-294-5
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28 AERELSE 34
                                             66 AERELSE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EREKEOM 7
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LENGTH: 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Sequence 8153, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NOS: 8344
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Patent No. 6610836
Patent No. 6610836
Patent No. 6610836
Patent No. CGLOBAD
Patent No. CGLOBAD
Patent No. CGLOBAD
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489, 039A
TITLE OF INVENTION: NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US/09/489, 039A
PRIOR RILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14059
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                   SEQ ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (22)
COHER INPORMATION: (22)
SUBSTITUTION: (22)
COHER INPORMATION: Xaa = tyrosine or a phosphorylated tyrosine
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.4%; Score 10; DB 4; Length 27; Best Local Similarity 100.0%; Pred. No. 0.0016; Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 249;
. 11;
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17.1%; Score 7; DB 4
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-8153
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LRLQDXEEKTK 26
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US-09-489-039A-14059
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GENERAL INFORMATION:
APPLICANT: WEBINAANN, ROBERTO
TITLE OF INVENTION: HUMAN HOMOLOGUE OF YEAST HELICASE AND USES THEREOF
FILE REFERENCE: db7 sequence
                  Gaps
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Sequence 144, Application US/09168595
Patent No. 655566
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 645;
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                  Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
Pred. No. 24;
Mismatches
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100.0%; Pred. No. 24;
tive 0; Mismatches
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ATORNEY/AGENT INFORMATION:
NAME: Sholtz. Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-011
TELECHONIC (A15) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO. 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09425335
Patent No. 6518052
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
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US-09-168-595-144
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amino acid
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Best Local Similarity 100.
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                                                                                            483 KAERELS 489
                                                        27 KAERELS 33
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
                                                                                                                                                   RESULT 8
US-09-168-595-144
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STATE: C.
COUNTRY:
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US-08-687-080-47
US-09-687-080-47
Sequence 47, Application US/08687080
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                              0; Indels
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEN PC compatible
COMPUTER: Patentin Pclease #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FLING DATE: 10-Jul-1996
CLASSIFICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
TELEBHONE: (415) 324,0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                      Score 7; DB 2; Pred. No. 24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 7;
                                                                                                                                                                                                                                                                                      17.1%; Scc...
100.0%; Pre
                  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INPORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
// INDIVIDUAL ISOLATE: G18.pep
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US-08-592-126-144
    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 645 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    Query Match 17.1
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                       483 KAERELS 489
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                                                                                                                                                                                                               CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
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                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Squence 148, Application US/08592126

Squence 148, Application US/08592126

Fatent No. 5821091

SAPILCANT: Gragory Dolganov

TITLE OF INVENTION: Transcripts Encoding Immunomodulatory

TITLE OF INVENTION: Polypeptides

NUMBER OF SEQUENCES: 151

CORRESPONDENCES: 151

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: A

COMPUTE: Palo Alto

STATE: Palo Alto

COMPUTE: Palo Alto

STATE: Palo Alto

COMPUTE: Palo Alto

STATE: Palo Alto

STATE: Palo Alto

COMPUTE: Palo Alto

STATE: Palo Alto

STATE: Palo Alto

COMPUTE: Palo Alto

STATE: PALOGRAPH

COMPUTE: READABLE FORM:

MEDIUM TYPE: BREEN: PC-DOS/MS-DOS

SOFTWARR: PREADABLE FORM:

SAPELICATION NUMBER: US/08/592,126

FILING DATE:

TALGATION NUMBER: APPLICATION NUMBER: US/08/592,126
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INDIVIDUAL ISOLATE: Rad50.pro-translation of SEQ ID NO:54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1312;
                                                                                                                                                                                                                                         17.1%; Score 7; DB 4; Length 689; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz. Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 324-0860
TELEFONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 148:
CURRENT APPLICATION NUMBER: US/09/425,335
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
                                                                                                                                                                                                                                              Query Match 17.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 KAERELS 489
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                                                                                                                                                                                                                                                                                                                                               13 ELMLRLQ 19
                                                                                                                                                                                                                                                                                                                                                                                           52 ELMLRLO 58
                                                                                                                                                    ; TYPE: PRT
; ORGANISM: HUMAN
US-09-425-335-2
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RESULT 11 US-08-687-080-51

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Sequence 51, Application US/08687080

Patent No. 5965427

GENERAL INFORMATION:
APPLICANT: Gregory bolganov
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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389 TO 4324
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                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
NEERRENCE/DOCKET NUMBER: 4600-0111.30
TELEBRACH IN NUMBER: 4600-0111.30
TELEBRACH (415) 324-0980
INDOMMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
ILBNOTH: 1312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.1%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: T
INDIVIDUAL ISOLATE: 3
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Gaps

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Sequence 6, Application US/08725027
Sequence 6, Application US/08725027
Patent No. 6251566
GENERAL INFORMATION:
APPLICANT: TOCKMAN, MELVYN, S.
APPLICANT: TOCKMAN, MELVYN, S.
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                           Length 12;
                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,027
FILING DATE: 02-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/725,027
FILING DATE: 02-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
RECESTRATION NUMBER: 2026-4201US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE (212) 758-4800
TELEFRANCE (212) 751-6849
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%; Score 6; DB 3
100.0%; Pred. No. 7.5
tive 0; Mismatches
                                                                                                                                                                             14.6%; Score 6; DB 2
100.0%; Pred. No. 7.5
rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MBDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 6, Conservative
  SEQUENCE CHARACTERISTICS:
                                             TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide US-08-725-027-6
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                                                                                                                                       US-08-538-711A-6
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US-08-725-027-6
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APPLICANT: MULSHINE, JAMES, L.

APPLICANT: MULSHINE, JAMES, L.

TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND

TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION

NUMBER OF SEQUENCES.3

CORRESPONDENCE ADDRESS:

ADDRESSER: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PRKR AVENUE

CITY: NEW YORK

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,595
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/592,126
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.1%; Score 7; DB 4;
100.0%; Pred. No. 45;
vative 0; Mismatches
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COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538,711A
FILING DATE: 0.2-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE: CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4201
TELECOMMUNICATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08538711A Patent No. 5994062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 KAERELS 489
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US-08-538-711A-6
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                        0; Indels
Length 12;
                                                                                                                  US-09-542-552-6; Sequence 6, Application US/09542552
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us-09-856-070b-29.oli.rai

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GENERAL INFORMATION:

APPLICANT: MULSHINE, JAMES, L.

TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
INVERSE OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
COUNTRY: USA
COMPUTER RADABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: BADDLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: ASCII
COMPUTER: 18M PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
FILING DATE: 03-APR-2000
CLASSIFICATION NUMBER: 08/538,711
FILING DATE: 02-OCT-1955
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 08/538,711
FILING DATE: 02-OCT-1955
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 2006
CLASSIFICATION NUMBER: 2006
CLASSIFICATION NUMBER: 2006
CLASSIFICATION NUMBER: 2006
TELECOMMOTICATION NUMBER: 2006
TELECOMMOTICATION NUMBER: 2006
TELECOMPOTION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TELECOMPOTION POR SEG ID NO: 6:
SEQUENCE CHARACTERISTICS:
TELECOMPOTION POR SEG ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Linear

MOLECULE TYPE: peptide
US-09-542-552-6
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Search completed: August 16, 2004, 09:57:43 Job time : 39 secs

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Gaps ;

0; Indels

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August 16, 2004, 09:56:08; Search time 46 Seconds (without alignments) 279.805 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Ggn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NBM_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NBM_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NBM_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_NBW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_NBM_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1292805 segs, 313927144 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4728, Ap	Sequence 117, App	Sequence 2372, Ap	Sequence 1160, Ap	Sequence 896, App	Sequence 896, App	Sequence 8, Appli	Sequence 232000,	Sequence 43920, A	Sequence 232005,	Seguence 45766, A	Sequence 232010,	Sequence 232009,	Sequence 55605, A	Sequence 56199, A	
SUMMARIES	ОП	US-10-106-698-4728	US-10-116-275-117	US-10-408-765A-2372	US-10-408-765A-1160	US-09-925-299-896	US-09-925-299-896	US-09-988-493-8	US-10-424-599-232000	US-10-425-114-43920	US-10-424-599-232005	US-10-425-114-45766	US-10-424-599-232010	US-10-424-599-232009	US-10-425-114-55605	US-10-425-114-56199	
	DB	14	15	16	16	σ	10	13	12	12	12	12	12	12	12	12	
	Query Match Length DB	436	586	586	630	635	635	80	105	170	207	207	298	391	408	408	
	Query Match	48.8	48.8	48.8	48.8	48.8	48.8	19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.5	
	Score	20	20	20	20	20	20	80	80	80	80	00	00	80	œ	60	
	Result No.	1	7	e	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	

Sequence 229552, Sequence 5, Appli Sequence 5, Appli Sequence 597, App Sequence 597, App Sequence 224, Appl Sequence 224, Appl Sequence 27, Appl Sequence 27, Appl Sequence 151, Appl Sequence 11, Appl Sequence 11, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 148, Appli	Sequence 136247, Sequence 136247, Sequence 372, App Sequence 53, Appl Sequence 226483,
2 US-10-424 US-09-848: US-10-108: US-10-108: US-10-108: US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-10-074 US-09-976- US-09-9	b US-10-43/-963-13 6 US-10-437-963-13 6 US-10-363-616-313 1 US-09-933-780C-5 2 US-10-424-599-22
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11111277777777777777777777777777777777	4 4 4 4 4 4 8 6 4 ቢ

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USECULATION OF THE PROPERTY OF THE PRIOR PRIOR APPLICATION NO. US20030109690A1

SEQUENCE AL THORNATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
FILE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
FRIOR PELING DATE: 2000-09-28
FRIOR PELING DATE: 1999-09-29
FRIOR APPLICATION NUMBER: US 60/157,137
FRIOR APPLICATION NUMBER: US 60/157,137
FRIOR APPLICATION NUMBER: US 60/163,280
FRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SEQ ID NO 4728
LINGUARE: 436
LENGTH: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (382)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.8%; Score 20; DB 14; Length 436;
.larity 100.0%; Pred. No. 2.1e-11;
Conservative 0; Mismatches 0; Indels
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Best Local Similarity
Matches 20; Conserv
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1 EREKEOMMREKEELMLRLOD 20

Gaps 0

184 EREKEÇMMREKEELMLRLQD 203

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Gaps
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; Sequence 896, Application US/09925299
; Patent No. US2002055627A1
; GENERAL INFORMATION:
; TILE APPLICANT: Rosen et al.
; TILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; TILE REFERENCE: PAIO2
CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR APPLICATION NUMBER: C0/124,270
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 896
; LENGTH: 635
                                                     APPLICANT: Zhang, Bing
APPLICANT: Glbson, Bradford W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Glenn, Cary M.
APPLICANT: Glenn, Cary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTECME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 630;
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Publication No. US20030040617A9;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PCT/US00/05883;
PRIOR FILING DATE: 2000-03-08
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48.8%; Score 20; DB 16;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 20; Conservative 0; Mismatches 0.
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APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-09-925-299-896
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US-09-925-299-896
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LENGTH: 630
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                                                                        Sequence 117, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, Dariel J.
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Lisa
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: B1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
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| Sequence 2372, Application US/10408765A
| Publication No. US20040101874A1
| General Information:
| APPLICANT Ghosh, Soumitra S. |
| APPLICANT Ghosh, Soumitra S. |
| APPLICANT Ghosn, Bradford W. |
| APPLICANT Glenn, Gary M. |
| APPLICANT Glenn, Gary M. |
| APPLICANT Glenn, Cary M. |
| APPLICANT Warnock, Dale B. |
| TITLE OF INVENTION IDENTIFIED IN THE MITOCHONDRIAL PROTEOME FILE REFERENCE: 660088 465 |
| CURRENT APPLICATION NUMBER OF SEQ ID NOS: 3077 |
| SOFTWARE PRESENCE FRANCE SOUR OF SEQ ID NOS: 3077 |
| SEQ ID NO 2372 |
| LENGTH: 586 |
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48.8%; Score 20; DB 16; Length 58
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

48.8%; Score 20; DB 15; I
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 0;
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; Sequence 1160, Application US/10408765A
; Publication No. US20040101874A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-116-275-117
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ORGANISM: Homo sapiens
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                                                                  US-10-116-275-117
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LENGTH: 586
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RESULT 4

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Sequence 232005, Application US/10424599

Publication No. US2004003107241

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: SON Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 232095

LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-425-114-43920
US-10-425-114-43920
Sequence 43920, Application US/10425114
Sequence 43920, Application US/10425114
Sequence 43920, Application No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Labaska, Jack
APPLICANT: Soreen, Steven E
APPLICANT: Soreen, Steven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (5313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 43920
LENTH: 170
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                                                                                       FEATURE:
// OTHER INFORMATION: Clone ID: PAT_MRT3847_51518C.1.pep
US-10-424-599-232000
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red. No. 3;
Mismatches
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100.0%; Pred. No. 4.5;
tive 0; Mismatches
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US-10-425-114-43920
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Pred. No.
                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 TKKAEREL 32
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                              TYPE: PRT
ORGANISM: Glycine max
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   LENGTH: 105
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Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Too Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 288684
SEQ ID NO 232000
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; Bublication No. US20030064419A1
; GENERAL INFORMATION:
APPLICANT: Herath Mudiyanselage Athula Chandrasiri
APPLICANT: O'Hare, Michael John
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Materfield, Michael Derek
CURRENT APPLICATION NUMBER: US/09/988,493
CURRENT APPLICATION NUMBER: PGT/GB01/01219
FRIOR APPLICATION NUMBER: GB 0006695.1
FRIOR APPLICATION NUMBER: GB 0007265.2
FRIOR FILING DATE: 2000-03-20
FRIOR 
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100.0%; Pred. No. c.
'... 0; Mismatches
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100.0%; Pred. No. 1.2
:ive 0; Mismatches
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1556 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 896 LENGTH: 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 EREKEÇMMREKEELMLRLQD 402
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                TYPE: PRT CORGANISM: Homo sapiens US-09-925-299-896
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ORGANISM: homo sapien
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Too Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Liu, Jingdong
APPLICANT: Screen, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Sucal Scree
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Local Similarity 100.0%; Pred. No. 9.4;
les 8; Conservative 0; Mismatches 0; Indels
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US-10-425-114-55605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_51526C.1.pep
US-10-424-599-232009
                                                                                                                                                                                                                                                                                                                                       ; Sequence 232009, Application US/10424599 ; Publication No. US20040031072A1
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                                                                                                                            257 TKKAEREL 264
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ORGANISM: Glycine max
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                                              25 TKKAEREL 32
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LENGTH: 391
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Sequence 45756, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Application Screen, Steven E

APPLICANT: APPLICANT: Go, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION STALES

SEQ ID NO 45766

LENGTH: 207
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Publication No. US20040031072A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE:
GENERAL APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE:
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    DB 12; Length 207; . 5.4;
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US-10-424-599-232010
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US-10-425-114-45766
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OTHER INFORMATION: unsure at all Xaa locations
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19.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 5.4
Matches 8; Conservative 0; Mismatches
Query Match 19.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 5.4
Matches 8; Conservative 0; Mismatches
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Matches 8; Conservative
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US-10-425-114-56199

Sequence 56199, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

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APPLICANT: Tabaska, Jack E

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack
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ezrin [validated]
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A, Accession: S09263 A, MoLecule type: mRNA A, Residues: 2-586 cGOU'> A, Cross-references: GB:X51521; NID:g31282; PIDN:CAA35893.1; PID:g31283

transcription repr similar to arsenat hypothetical prote flagellar basal bo robable thioredoxi probable thioredoxi probable thioredox thioredoxin 2 [imp hypothetical prote hypothetical prote H-transporting tw petP protein - Rho protein F47F6.4 [i ribosome recycling conserved hypothet gene sj22 protein	₽	t-1996 #text_change 24-Nov-2003 , R.S.; Nestler, E.J. associated with cell shape and growth, are e	lated from GB/EMBL/DDBJ 8; NID:9289407; PIDN:AAA30510.1; PID:9288408 //moesin family; protein 4.1 membrane-binding domain homology membrane-binding domain homology <b41></b41>	DB 2; Length 581; 2.8e-12; .hes 0; Indels 0; Gaps 0;	•
H82197 B96951 P90024 P900251 E65036 G859036 G859036 G859036 G859036 H691659 F69160 F69160 F69160 F69160 F69160 F69160 F69160 F69160 F691735 F691735 F691735	ALIGNMENTS	genius taurus (cattle) #sequence_revision 15-Oct-1996 io, H.; Saijoh, K.; Duman, R.S. 4, 64-73, 1993 ssteonectin, two proteins assoc 145889		Score 20; DB; Pred. No. 2. 0; Mismatches	QD 20
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11111111111111111111111111111111111111		tius ta equence H.; Sa 64-73 eonecti	translated .M98498; NII adixin/moesi	vat	REKEELM
<pre></pre>		primigenius taurus 1996 #sequence_revi 5889	inary; mRNA 11 <ber: 68:="" gb="" re<="" td="" zrin=""><td>ilarity Conse</td><td>BREKEOMMREKEELMLRLOD </td></ber:>	ilarity Conse	BREKEOMMREKEELMLRLOD
νωνυνουνουνουο		os p ct-1 145 .M.; eurc	elia elia ype: 1-58 renc renc in:	հ Տiա 20;	₹#
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A, Molecule type: protein
A, Residues: 53-57,149, L',150, 'G',152-155 < EG3>
A, Residues: 53-57,149, L',150, 'G',152-155 < EG3>
A, Residues: 53-57,149, L',150, 'G', 152-155 < EG3>
A, Residues: 63-57,149, L',150, 'G', 152-155 < EG3>
A, Fexperimental source: WRL lpr/lpr, T-cells
A, Note: sequence extracted from NGB1 backbone (NCBIP:112940)
C, Superfamily: exrin/radixin/meesin family; protein 4.1 membrane-binding domain homology
C, Superfamily: exrin #steatus predicted *MAT>
F, 2-586/product: exrin #steatus predicted *MAT>
F, 7-291/Domain: protein 4.1 membrane-binding domain homology < E841>
F, 7-291/Domain: actin binding #status predicted
F, 66/Binding site: phosphate (Ser) (covalent) #status predicted
F, 66/Binding site: phosphate (Thr) (covalent) #status predicted
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                                                R;Egerton, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Bretscher, A.; Samelson, L.E.
J. Immunol. 149, 1847-1852, 1992
A;Title: Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein in T cells.
A;Reference number: A46501; WUID:92388649; PMID:1381389
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A;Residues: 1-142 <STO>
A;Cross-references: GB:AE005172; NID:g11079495; PIDN:AAG29206.1; GSPDB:GN00141
C;Genetics:
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A,Cross-references: EMBL:X60671; NID:g50880; PIDN:CAA43086.1; PID:g50881
R;Egerton, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Bretscher, A.; Sam
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Pred. No. 0.00026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Status: preliminary
A,Molecule type: protein
A,Reseluce: 27-33, E' <EG2>
A,Experimental source: MRL lpr/lpr, T-cells
A,Note: sequence extracted from NCBI backbone (NCBIP:112936)
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: MRL lpr/lpr, T-cells
A;Note: sequence_extracted from NCBI backbone (NCBIP:112938)
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100.0%; Pred. No.
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Conservative 0;
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 412-426 <EGE>
A;Experimental source: MRL
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les 7; Conserv
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A;Status: preliminary
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              R;Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; delectrophoresis 11, 528-536, 1990
Bjectrophoresis 11, 528-536, 1990
A;Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencin A;Reference number: A61002; MUID:91031404; PMID:1699755
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:120489; OMIM:123900
A;Map position: 6q25-6q26
C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
C;Keywords: actin binding; cytoskeleton; membrane-associated protein; phosphoprotein
F;2-56/Froduct: ezrin #status experimental <MMT>
F;7-51/bomain: protein 4.1 membrane-binding Ammi-
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                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 255-263;194,'Q',196-199,'X',201;264-270 cBAU>
A,Residues: 255-263;194,'Q',196-199,'X',201;264-270 cBAU>
A,Note: it is not certain whether this material represents ezrin or radixin (see entry PA;Note: this material corresponds to transformed epithelial amnion cell (AMA) database [C,Comment: This protein is located in microvilli and is proposed to play a role in modul C;Genetics:
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Cibacte: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 24-Nov-2003
Cibacte: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 24-Nov-2003
Cibaccession: T4717
Sibacterwaelder, B.; Obermaier, B.; Mewes, H.W.; Weil, B.; Wiemann, S.
Aibacteric to the Protein Sequence Database, March 2000
Aibacteric number: 224377
Aibaccession: T47177
Aibaccess
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F;55-286/Region: actin binding #status predicted
F;65B-286/Region: actin binding #status predicted
F;65B-101 site: phosphate (Sex) (covalent) #status predicted
F;214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted
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48.8%; Score 20; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-586 <FUN>
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Best Loca Matches

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DNA-binding protein, fatty acid/fatty acyl-responsive - Escherichia coli (strain O157:H7, C.Species: Eacherichia coli (c.Species: Bacherichia coli (c.Species: Bacherichia) (c.Species: Bacherichia coli (c.Species: Bacherichia) (c.Species: Bacheric
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A,Residues: 1-239 <STO-
A,Cross-references: GB.A.B.D005174; NID:g12514884; PIDN:AAG56038.1; GSPDB:GN00145; UWGP:Z19:
A,Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-Dunding protein, fatty acid/fatty acyl-responsive - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (cjatte: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 19-Jul-2002 C;Accession: BB5697 B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                  A;Residues: 1-239 <KUR>
A;Residues: 1-239 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC90954.1; PID:g15980150; GSFDB:GN00175
C;Genetics:
A;Gene: fadR
C;Superfamily: pyruvate dehydrogenase complex repressor
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C;Superfamily: pyruvate dehydrogenase complex repressor
                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 7; DB 2; ilarity 100.0%; Pred. No. 12; Conservative 0; Mismatches
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100.0%; Pred. No. 12;
cive 0; Mismatches
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nes 7; Conservat
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A;Status: preliminary
A; Molecule type: DNA
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Matches
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                                                                                                                                                                                   DNA-Dinding protein, fatty acid/fatty acyl-responsive - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Species: Date: 10-Sep-1999 #sext_change 19-Jul-2002 C;Species: 10-Sep-1999 #sext_change 19-Jul-2002 C;Species: 10-Sep-1999 #sext_change 19-Jul-2002 C;Species: 10-Sep-1999 #sext_change 19-Jul-2002 R;Blattner, F.R.; Plunkett III, G;Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc, A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64864
A;Accession
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A. Description: represses transcription of at least eight genes required for fatty acid the biosynthesis; activates the iclR gene encoding the transcription regulator of the aceBAK A. Pathway: fatty acid metabolism
A. Note: fadR-dependent DNA binding and transcriptional activation is prevented by long controls.
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Nucleic Acids Res. 16, 7995-8009, 1988
A.Title: Nucleotide sequence of the fadR gene, a multifunctional regulator of fatty acid
A.Reference number: S01288; MUID:88335542; PMID:2843809
A.Accession: S01288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A) Residues: 1146, Tr, 148-239 <DIR>
A) Cross-references: ENBL.X08087; NID:g992990; PID:g992991
A) Cross-references: ENBL.X08087; NID:g992990; PID:g992991
A) Experimental source: strain K-12
A) Note: the author translated the codon ACC for residue 147 as Asn
R; DiRusso, C.C.; Helmert, T.L.; Netzger, A.K.
J. BAOL: Chem. 267, 8685-8691, 1992
A) Title: Characterization of FadR, a global transcriptional regulator of fatty acid meta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-239 <BLAT>
A;Cross-references: GB:AE000217; GB:U00096; NID:g1787434; PIDN:AAC74271.1; PID:g1787436;
A;Experimental source: strain K-12, substrain MG1655
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C;Keywords: DNA binding; homodimer; transcription regulation
F;31-55/Region: helix-turn-helix motif
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A;Accession: A38103
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-11 cDI2>
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100.0%; Pred. No. 12;
iive 0; Mismatches
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Best Local Similarity 100.
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A;Gene: fadR; oleR; thdB
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                                        Length 239;
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C; Superfamily: pyruvate dehydrogenase complex repressor
                                      Query Match 17.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 12; Matches 7; Conservative 0; Mismatches
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33 AERELSE 39

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RESULT 10

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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. surrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Reference number: A99139
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     horserine kinase (thrB) [imported] - Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
C.Species: Sulfolobus solfataricus
C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C.Accession: G90407
R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A.Description: Sulfolobus solfataricus complete genome.
A.Reference number: A99139
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A;Experimental source: strain 972h-; cosmid c947
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A,Residues: 1-303 <KUR>
A,Cross-references: GB:AE006641; NID:g13816366; PIDN:AAK43085.1; GSPDB:GN00155
C,Genetics:
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A,Molecule type: DNA
A,Residues: 1-311 <KUR>
A,Cross-references: GB:AE006641; NID:g13815670; PIDN:AAK42518.1; GSPDB:GN00155
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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K;Lyra, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21884
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A,Status: preliminary; translated from GB/EMBL/DDBJA,Molecule type: DNA
A,Residues: 1-452 < LIYN>
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100.0%; Pred. No. 15;
tive 0; Mismatches
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C;Superfamily: homoserine kinase
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Best Local Similarity 100.0
Matches 7; Conservative
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A;Gene: SPDB:SPBC947.13
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                                                                                                                                                                                                       Accession: B2214. B221. Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. R. R., Rikalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A,71tle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD:20406833; PMID:10952301
A;Accession: B8214A
A;Accession: B8214A
A;Accession: B8214B
A;Accession: B8314B
A;Acces
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A;Moteule type: DNA
A;Residues: 1-239 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05488.1; PID:g16502992; GSPDB:GN00176
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: F90478
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A;Gene: VC1900
A;Map position: 1
C;Superfamily: pyruvate dehydrogenase complex repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: STY1934
C;Superfamily: pyruvate dehydrogenase complex repressor
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33 AERELSE 39

RESULT 11

28 AERELSE 34

A; Accession: AF0723

C;Genetics:

Query Match
Best Local Similarity 100.
Matches 7; Conservative

28 AERELSE 34

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AERELSE 39

RESULT 12 F90478

Pred. No. 20;

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completed: August 16, 2004, 09:56:52
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A, Status: preliminary
A, Accession: S66049
A, Status: preliminary
A, Molecule type: DNA
C, Molecule type: DNA
C, Brunich, S.D.; Bruschi, C.V.; Caldwell, B.A.; Alebret, C.; Ferrari, E.
Nature 390, 249-256, 1997
Nature 390, 249-256, 1997
Nature 390, 249-256, 1997
A, Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A, Multors: Roulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A, Authors: Lauber, J.; Lazaravic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masudel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon,
A, Authors: Solleich, S.; Schrocter, P.; Roshika, N.; Tosato, V.; Voshika, R.;
A, Authors: Yoshikawa, H.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.
A, Authors: Yoshikawa, H.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.
A, Althors: Yoshikawa, H.; Danchin, A.
A, Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A, Accession: B69518
                                                                                                                                                                                                                                                                                                                                                   MACHACITY BACKLORY DOLYMERASE (EC 2.7.7.7) III chain dnax - Bacillus subtilis NA-directed DNA polymerase (EC 2.7.7.7) III chain dnax - Bacillus subtilis by Alternate names: DNA polymerase III (gamma and tau subunits) dnax c;Species: Bacillus subtilis subtilis subtilis corrected in the subtilis subtilis subtilis subtilis subtilis subtilis subtilis S60745; S66049; B69618 R;Alonso, J.C.; Shirahige, K.; Ogasawara, N. R;Alonso, J.C.; Shirahige, K.; Ogasawara, N. A;Title: Molecular cloning, genetic characterization and DNA sequence analysis of the reparence number: S13786; MUID:91088245; PMID:2124672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: EMBL:X17014; NID:9453238; PIDN:CAA34877.1; PID:9580914
R.Struck, J.C.R.; Vogel, D.W.; Ulbrich, N.; Erdmann, V.A.
Nucleic Acids Res. 16, 2720, 1988
A.Title: A diazx-like open reading frame downstream from the Bacillus subtilis scRNA gen
A.Reference number: S00745; MUID:88203213; PMID:2452406
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A Residues: 1-422 «STR»
A;Cross-references: EMBL:X06803; NID:g39891; PIDN:CAA29958.1; PID:g580855
R;Cgasawara, N.; Nakai, S.; Yoshikawa, H.
B;Cgasawara, I. 1-14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom
A;Reference number: S65967; MUID:96051385; PMID:7584024
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A;Experimental source: strain 168
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A,Start codon: GTG
C,Superfamily: DNA-directed DNA polymerase III gamma chain
C,Keywords: nucleotidyltransferase
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100.0%; Pred. No. 25;
tive 0; Mismatches
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            Best Local Similarity 100.0%; P. Matches 7; Conservative 0;
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Matches 7; Conservative
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A;Residues: 1-563 <ALO>
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thermoanaer bacillus ca methanobact bacillus ps rhodobacter

P33636 Q8rb52 P41014 Q50521 P09221 P31078

escherichia

bordetella bordetella bordetella rickettsia

07wqs9 07w1v3 07vs88 09ze08 P77181

escherichia

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Kidney;
MEDLINE-96239137; PubMed=8660651;
MEDLINE-96239137; PubMed=8660651;
Galat A., Garbod M.C., Bouet F., Riviere S.;
Galat A., Garbod M.C., Bouet F., Riviere S.;
and applications.";
Arch. Biochem. Biophys. 330:229-237(1996).
-:- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-:- SUBCELIULAR LOCATION: Microvillar peripheral membrane protein
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

TISSUB-Brain; Zhao H., Saijoh K., Duman R.S., Nestler E.J.;

Berggon C.M., Zhao H., saijoh K., Duman R.S., Nestler E.J.;

Egrin and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus.";
                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Skaryota Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinne; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                         ALIGNMENTS
FIGB AQUAE
THI2 ECOLI
Y972 THETR
ATPP BACCA
YB48 METTW
ATPF BACP3
PETF RHOCA
DEFI BORBA
DEFI BORBA
DEFI BORBA
RHOCA
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BORPE
BORPE
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PIR; 145899; 145889.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000198; Ex/rad/moesin.
InterPro; IPR0009954; Moesin.
Pfam; PF00759; Band 41; 1.
Pfam; PF00769; EMN, 1.
PRNYE; SM00295; BAND41.
SMART; SM00295; B41; 1.
PROSITE; PS00660; PERM_1; 1.
PROSITE; PS00660; PERM_2; 1.
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                                                                                                                       PAAY
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  124
1128
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  NCBI_TaxID=9913;
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ID EZRI BOVIN
AC P31976;
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459786017845
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mus musculu
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                                                                               August 16, 2004, 09:52:02; Search time 32 Seconds (without alignments) 66.715 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                        141681 segs, 52070155 residues
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NOES_RAI
NOES_RAI
RADI HUWAN
RADI HUWAN
RADI WOUSE
RADI PIG
EZRI RABIT
RPC MOUSE
RPC MOUSE
RPC MOUSE
RPCM SCHPO
AKII RAI
HDAG WOUSE
HDAG HUWAN
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RSR1_VIBCH
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EZRI HWAN
EZRI HWAN
EZRI MOUSE
FADR SALTI
FADR SALTI
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TREPA
STRMU
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                                                             OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                         US-09-856-070B-29
                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                     Sequence:
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Perfect 8
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fication of ezrin as an 81-kDa tyrosine-phosphorylated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Immunol. 149:1847-1852(1992).
-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-!- SUBCELLULAR LOCATION: Microvillar peripheral membrane protein
                                                                                SEQUENCE OF 171-179 AND 342-349.
MEDLINE=99311348; PubMed=8713105;
SESTEON M., Moritz R.L., Druker B., Kelso A., Simpson R.J.;
"Identification of the 70kD heat shock cognate protein (Hsc70) and alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (cytoplasmic side).
                                                                                                                                                                                                                                                                                                                                                                  Krieg J., Hunter T.;
"Identification of the two major epidermal growth factor-induced
tyrosine phosphorylation sites in the microvillar core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural protein; CyToskeleton; Phosphorylation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92388649; PubMed=1381389;
Egerton M., Burgess W.H., Chen D., Druker B.J., Bretscher A.,
Samelson L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1, Length 585;
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2A844D140E3B06CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: Phosphorylated by tyrosine-protein kinases.
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 224:666-674(1996).
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InterPro: IPR000399; EZ/rad/mocein.
InterPro: IPR000399; EZ/rad/mocein.
InterPro: IPR000994; Mocsin.
Pfam; PF00373; Band 41; 1.
PRINTS; PR00965; EM1; 1.
PRNSTITE; SM00295; B41; 1.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00660; FERM 3; 1.
PROSITE; PS00661; FERM 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 267:19258-19265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; JOS021; AAAG1278.1; ALT INIT.
EMBL; AL162086; CAB82418.1; ALT_INIT.
EMBL; BC013903; AAH13903.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٨
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SWISS-2DPAGE; P15311; HUMAN.
                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION BY PDGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:12691; VIL2.
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PDB; 1NI2; 25-FEB-0
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AN EMELINE-2234648; FUDNGG-12466851;

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

A Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Baldarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Farsegawa Y., Nogami A., Schonbach C., Gojobori I.,

Baldare J., Bradt D., Brusto V., Chochia C., Corbai L.E., Cousins S.,

Baldare J., Pragani T.A., Fletcher C.F., Forrest A., Frazer K.W.

A Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.W.

A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

A Majoltt D.R., Maltais L., Marchionni L., Mokenzie L., Mixi H.,

A Nagabima T., Numata K., Okido T., Partad B., Lyons P.A.,

A Rawai T., Reed J.C., Reed D.J., Reid J., Ramachandran S.,

A Sandelin A., Schneider C., Sendol M., Shimada K.,

A Sandelin A., Schneider C., Sendol M., Shimada K.,

A Verardo R., Wanner L., Wahlestedt C., Wann Y., Yang I., Yang L.,

A Verardo R., Wanner L., Wahlestedt C., Wann Y., Yang I., Yang L.,

A Wilming L.G., Wynshaw-Boris A., Yanaglawa M., Sakazume N., Sakazume N.,

A Shiraki T., Waki K., Kawai J., Alzawa K., Arakwa T., Fukuda S.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itch M., Kagawa I.,

A Minanshi A., Soshino M., Waterston R., Lander E.S., Shinagawa A.,

Bantey B., Hayshiazki Y., Wanner H., Jander E.S., Shinagawa A.,

Bantey B., Mannishi A., Yoshino M., Waterston R., Shinagawa A.,

Bantey B., Mannishi A., Washiazki M., Shinata M., Shinagawa A.,

Bantey B., Mannishi A., Washino M., Waterston R., Shinagawa A.,

Bantaya M., Mannishi A., Washino M., Waterston R., Shinagawa A.,

Bantaya M., Mannishi A., Washino M., Waterston R., Shinagawa A.,

Bantaya M., Mannishi A., Washino M., Waterston R., Shinagawa A.,

Bantaya M., Mannishi A., Washino M., Waterston R., Shinagawa M., Mannishi A., Washino M., Waterston R., Shinagawa M., Mannishi A., Washino M., Waterston R., S
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Analysis of the mouse transcriptome based on functional annotation of
6,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINB=22388257; PubMed=12477932;
Strauberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Strauberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdáin T.B., Tobhiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellando N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                 Indels
         Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                 EZRI_MOUSE STANDARD; PRT; 585 AA. P26040; Q80ZT8; Q9DCI1; Created) 10-OAY-2003 (Rel. 22, Created) 10-OAY-2003 (Rel. 42, Last sequence update) 10-OAT-2004 (Rel. 43, Last annotation update) Ezrin (p81) (Cytovillin) (Villin 2).
                                 Mismatches
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STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=22354683; PubMed=12466851;
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                                                                                            1 EREKEOMMREKEELMLRLQD 20
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                                    20; Conservative
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Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
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FADE ECOLI STANDARD; PRT; 238 AA.

10.90371; P76827;

10.1-MAR-1989 (Rel. 13, Last sequence update)

10.0CT-2003 (Rel. 42, Last annocation update)

Fatty acid metabolism regulator protein.

FADE OR DER OR THDB OR B1187 OR C1635 OR ECS1682 OR SF1176

OR S1264.
                                                                                                                                                                                                                                                           and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Probably involved in connections of major cytoskeletal
structures to the plasma membrane.
-!- SUBCELLUAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Component of the microvilli of intestinal
epithelial cells.
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Q -> P (IN REF. 1).

T -> A (IN REF. 1).

Q -> R (IN REF. 2).

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0 BY SIMILARITY.
294 FERM.
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EMBL; AK002766; BAB2341.1; -.
EMBL; BC49181; AA448181.2; -.
PIR; B41129; B41129.
MGD; MAI:98931, Vil.29.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000799; Bz/rad/moesin.
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SMART; SM00295; B41; 1.
PROSITE; PS00660; FERM_1; 1.
PROSITE; PS00661; FERM_2; 1.
PROSITE; PS0057; FERM_3; 1.
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Pfam; PF00769; ERM; 1.
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enterohemorrhagic Escherichia

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genome sequence of
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SPECIESE.coli, STRAIN=K12;
SPECIESE.coli, STRAIN=K12;
SPECIESE.coli, STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Itemoto K., Inada T., Itoh T., Kajihara M., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Kimura S., Kitagawa M., Makino K., Mashimoto H., Nishio Y., Saito N.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Yamamoto Y.,
Mori H., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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SPECIESE.C.O.01; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence of the fadR gene, a multifunctional regulator of fatty acid metabolism in Escherichia coli."; Nucleic Acids Res. 16:7995-8009(1988).
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SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=22386234; PubMed=12471157;
MEDLINE=22386234; PubMed=12471157;
MELOK R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.I.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic_structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIESE. 201); STRAIN=KI2 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Klay M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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Nature 409:529-533(2001).
                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xano m., norlucul 1.;
14 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
                                                                                                                                   Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                        SPECIES=E.coli; STRAIN=K12;
MEDLINE=88335542; Pubmed=2843809;
Escherichia coli 06,
Escherichia coli 0157:H7, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=E.coli; STRAIN=K12;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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WELLES TALLOGRAPHY (1.5 ANGSTROMS).

WELLES 21264500; PubMed=11279025;

X. W. Y., Heath R.J., Li Z., Rock C.O., White S.W.;

X. W. The FadR.DNA complex. Transcriptional control of fatty acid

The FadR.DNA complex. Transcriptional control of fatty acid

T. Biol. Chem. 276:17373-17379 (2001).

J. Biol. Chem. 276:17373-17379 (2001).

C. I. FUNCTION: Multifunctional regulator of fatty acid metabolism.

Represes transcription of at least eight genes required for fatty

acid transport and beta-oxidation among which fadA, fadB, fadD,

fadd and fadB. Activates transcription of at least three genes

cequired for unsaturated fatty acid biosynthesis: fabA, fabB and

iclR, the gene encoding the transcriptional regulator of the

aceBAK operon encoding the synsoritional regulator of the

fadR is specifically inhibited by long chain fatty acyl-CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157.", Nucleic Acids Res. 30:4432-4441(2002),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES Sflexmeri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Shen J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21192039; PubMed=11296236; van Aalten D.M., DiRusso C.C., Knudsen J.; "The structural basis of acyl coenzyme A-dependent regulation of the
                                                                                                                                                                                                                                                          Dirusso C.C., Heimert T.L., Metzger A.K., "Characterization of FadR, a global transcriptional regulator of fatty acid metabolism in Bscherichia coli. Interaction with the promoter is prevented by long chain fatty acyl coenzyme A.", J. Biol. Chem. 267:8685-8691(1992).
comparison with a laboratory strain K-12.";
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-!- SUBJUNIT: Homodimer.
-!- DOMA.IN: The C-terminal domain bind acyl-CoA.
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
                                                                                                                                    PARTIAL SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
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J. Biol. Chem. 272:30645-30650(1997)
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                                                                                                                                                                                   SPECIES=E.coli;
MEDLINE=92235103; PubMed=1569108;
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EMBO J. 20:2041-2050(2001).
    0157:H7 and genomic com
DNA Res. 8:11-22(2001).
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CHARACTERIZATION.
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Nature 413:848-852(2001).
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Q8ZPI5;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PDB; 1HW1; 06-UUN-01.
PDB; 1HW2; 04-UUN-01.
PCGGne; EG10281; FadR.
InterPro; 1PR00920; FadR.C.
InterPro; 1PR000524; HTH-GntR.
PFININS; PR00035; HTHGWTR.
SWART; SW00345; HTH GNTR; 1.
PROSTIT; PS00043; HTH GNTR; 1.
PROSTIT; PROMO ACTIVATOR; Repressor;
PRILY, acid metabolism; Transcription regulation; Activator; Repressor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
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1 70 HTH GNTR-TYPE.

33 52 H-T-H MOTIF (POTENTIAL).

238 AA, 26837 MW, ADASB06B7633197E CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Fatty acid metabolism regulator protein.
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding; Complete proteome; 3D-structure.
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100.0%; Pred. No. 7;
tive 0; Mismatches
                                                                                                                                                                                                                                            EMBL; AE016759; AAN80100.1; --
EMBL; AE016759; AAG56038.1; --
EMBL; AE002555; BAB35105.1; --
EMBL; AE015144; AAN42791.1; ALT_INIT.
EMBL; AE015982; AAP16682.1; --
PIR; B99839; B99839.
PIR; H64864; H64864.
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                                                                                                                                                         EMBL; X08087; CAA30881.1; -.
EMBL; AAC74271.1; -.
EMBL; D90753; BAA36042.1; -.
EMBL; D90752; BAA36034.1; -.
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Matches 7; Conservative
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ID FADR SALTI
AC Q8Z685;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO 0931;

MEDLINE=22531367; PubMed=1264504;

A Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

A Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

A Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

The comparative genomics of Salmonella enterica serovar Typhi strains Ty2

A Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

The consequence of Salmonella enterica serovar Typhi strains Ty2

A Deng W., Liou S.-R., Schwartz D.C., Blattner F.R.,

The compounds W. Schwartz D.C., Blattner F.R., Radb, fadb, and the gene encoding the transcription of at least eight, fadb, fadb and iclR, the gene encoding the transcriptional regulator of the caceBAK operon encoding the glyoxylate shunt enzymes. Binding of fadR is specifically inhibted by long chain fatty acyl-CoA compounds (By similarity).

C --- SUBGELLULAR LOCATION: Cytoplesmic (Potential).

C --- SUBGELLULAR LOCATION: Cytoplesmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PR00035; HTHGNTR.
SMART; SM00345; HTH GNTR; 1.
SMOSTTE; PS00043; HTH GNTR; PAMILY; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor; DNA-binding; Complete proteome.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Fatty acid metabolism regulator protein.
FapR OR STM1805.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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33 52 H-T-H MOTIF (POTENTIAL).
238 AA, 26802 MW, 9E7ESBTDE6F72CB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.1%; Score 7; DB 1
100.0%; Pred. No. 7;
tive 0; Mismatches
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL627272; CAD05488.1; -. EMBL; AE016837; AAC68738.1; -. HAMAP; MF_00696; -; 1. InterPro; IPR008220; FadR C. InterPro; IPR000524; HTH_GntR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100 18s 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 AERELSE 34
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FADR SHEON Q8ED80;
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SEQUENCE
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FADR SHEON
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                    Pfam; PF0032; gntR; 1.
PRINTS; PR0035; HTHGATR.
SMART; SM00345; HTT GNTR; 1.
PROSITE; PS00043; HTT GNTR; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor; DNA-binding; Complete proteome.
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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STRAIN=CO-92 / Biovar Orientalis;
MEDLINE-14704131 PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae; Yersinia.
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238 AA; 26855 MW; C464FADCFCE68DAA CRC64;
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BY SIMILARITY.
HTH GNTR-TYPE.
H-T-H MOTIF (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
EALY acid metabolism regulator protein.
FADR OR YF02144 OR Y2177
                                                                                                                                                                                                                                                                                                                     HAMAP) MF 00696; -; 1.
InterPro; IPR008920; FadR C.
InterPro; IPR000524; HTH_GntR.
                                                                                                                                                                                                                                                                                                     EMBL; AE008780; AAL20720.1; -.
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SEQUENCE
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Q8ZEL9;
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33 52 H-T-H MOTIF (POTENTIAL).
238 AA; 26770 NW; 27C0885E9767BCD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Fatty acid metabolism regulator protein.
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100.0%; Pred. No. ',
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
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Best Local Similarity 100..
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=670;
[1]
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100.0%; Pred
0; M
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InterPro; IPR008920; FadR C.
InterPro; IPR000524; HTH GntR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483(2000)
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es 7; Conserv
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SEQUENCE
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SO DER NOTE DE LE COURTE DE LE COURTE DE LE COURTE DE LE COURT DE 
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PROSTRIS, PS00043; HTH GNTR FAMILY; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor; DNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                 Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Musller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella Oneidensis."
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                                          Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBDATT: Homodimer (By similarity),
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
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Vibrionaceae; Vibrio.
NCBI TaxID=666;
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H-T-H MOTIF (POTENTIAL).
; 0EA97D59D7A15EBA CRC64;
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fatty acid metabolism regulator protein.
FADR OR VC1900.
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                                                                                                                                                                                                                                                                                          STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
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InterPro; IPR008920; FadR C.
InterPro; IPR00824; HTH_GntR.
Pfam; PF00392; gntR; 1.
PRINTS; PR00035; HTHGNTR.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=70863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
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            OR S02885
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SEQUENCE
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PRINUS; PR000325; HTHGNTR.
SMART; SM00345; HTH GNTR; 1.
PROSITE; PS00043; HTH GNTR; FAMILY; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor; Patty acid metabolism; Hardense proteome.
DNA-binding; Complete proteome.
HTH GNTR-TYPE.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIREI TOT Ni6961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Faft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: Multifunctional regulator of fatty acid metabolism (By
MEDLINE=22450551; PubMed=12562793;
Herz K., Vimont S., Padan E., Berche P.;
"Roles of NhaA, NhaB, and NhaD Na+/H+ antiporters in survival of
Vibrio cholerae in a saline environment.";
J. Bacteriol. 185:1236-1244(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
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-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 279;
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34 S3 H-T-H MOTIF (POTENTIAL).
279 AA, 31997 MW, 47D710A53CC4F5B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FADR. VIBPA STANDARD; PRT; 279 AA. 067N05; 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Fatry acid metabolism regulator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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Matches

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HAMAP; MF 00384; -; 1.
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SEQUENCE
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KHSE SULSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSTIRS, PS00043; HTH GNTR FAMILY; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor;
DNA-binding; Complete protecome.
                                      MEDLINE=22008454; PubMed=12620739; Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholezae."; Lancet 361:743-749(2003).

-: - FUNCTION: Multifunctional regulator of fatty acid metabolism (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Multifunctional regulator of fatty acid metabolism (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                  similarity).
-!- SUBURIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SUMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBL_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 279;
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32069 MW; 8429B92B45149399 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
16-OCT-2003 (Rel. 42, Last annotation update)
FADR OR VVI2233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7; I
Pred. No.
SEQUENCE FROM N.A.
STRAIN-RIMD 2210633 / Serotype 03:K6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00696; -; 1.
InterPro; 1PR008920; FadR_C.
InterPro; IPR00524; HTH_GhTR.
Pfam; PF00392; gntR; 1.
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100.08;
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Best Local Similarity 100...
Try Conservative
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279 AA;
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DNA BIND
SEQUENCE
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FADR VIBVU
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

STRAINE-ATCC 35092 / DSM 1617 / P2;

MEDLINE-2133296; DubMed=11427766;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-wehher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

The Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolbus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(12001).

-!- CATALYTIC ACTIVITY: ATP + L-homoserine = ADP + O-phospho-L-
                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00696; -; 1.
InterPro; IPR008920; FadR C.
InterPro; IPR008921; HTH_GntR.
Pfam; PF00392; gntR; 1.
PRINTS; PR0035; HTHGNTR.
SMART; SM00345; HTH GNTR; 1.
FALS FELS PR00315; HTH GNTR; 1.
FALS TANGORIE; PS00041; HTH GNTR FAMILY; 1.
FALS acid metabolism; Transcription regulation; Activator; Repressor; DNA-binding; Complete protecome.
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-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the GHMP kinase family. Homoserine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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17.1%; Score 7; DB 1; Length 279;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 1 1 1 HTH GNTR-TYPE.

34 53 H-T-H MOTIF (POTENTIAL).

279 AA, 32072 MW, 733F71C9F1167477 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homoserine kinase (EC 2.7.1.39) (HK).
                                                                                                                                                                                                                                                                                   EMBL; AE016804; AA010613.1; -.
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SOLUTION SOLUTION SERVICE SERV
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96051385; PubMed=7584024;
Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus
subtilis chromosome containing the replication origin.";
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        InterPro; IPR006203; GHMPknse ATP.
InterPro; IPR00870; Homoser_Kin.
Fram, PR00288; GHMP kinases; I.
FRIMS; PR00958; HOMSERKINASE; I.
TIGRFAMS; TIGR00191; thrB; 1.
THRFAMS; TIGR00191; thrB; 1.
Threonine blosynthesis; Transferase; Kinase; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                               Length 311;
                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                       SEQUENCE 311 AA; 33649 MW; 4E39A20E5F83D507 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
DNA polymerase III subunit gamma/tau (BC 2.7.7.7).
DNAX ON DNAH OR BSU00190.
                                                                                                                                                                                                                                                                                                                 DB 1;
.8.7;
                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 AA.
                                                                                                                                                                                                                                                                                                                 Query Match
17.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 8.7
Matches 7; Conservative 0; Mismatches
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                      ATP
  InterPro; IPR006204; GHMP_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                      98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EEKTKKA 187
                                                                                                                                                                                                                                                                                                                                                                                                                         22 EEKTKKA 28
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SEQUENCE FROM N.A.
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P09122;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII' complex. PolIII' associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Vanater D., Tognoni A., Viati A., Wandenbol M., Vannier F., Vassarotti A., Viati A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamanoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     Struck J.C.R., Vogel D.W., Ulbrich N., Erdmann V.A.; "A dnaZX-like open reading frame downstream from the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase, DNA-directed DNA polymerase, DNA replication, ATP-binding, Complete proteome.
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H -> D (IN REF. 2 AND 3).
; 2BA428D32B8DC35C CRC64;
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100.0%; Pred. No. 14;
tive 0; Mismatches
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EMBL, D26185; BAA6525.1; --
EMBL, Z69104; CAB11795.1; --
EMBL, X06803; CAA29958.1; --
EMBL, X52144; CAA36390.1; --
PIR; 1140469; I40469.
PIR; 113786; S13786.
Subcilist; BG10083; dnaX.
InterPro; IPR0035959; AAA_ATPase.
InterPro; IPR001270; Chaprin clpA/B.
InterPro; IPR001270; Chaprin clpA/B.
InterPro; IPR009821; P01 clampload_C.
InterPro; IPR009821; P01 clampload_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   subtilis scRNA gene.";
Nucleic Acids Res. 16:2720-2720(1988).
                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
MEDLINE=88203213; PubMed=2452406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91002681; PubMed=1698458;
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PRINTS; PR00300; CLPPROTEASEA.
                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-422 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-5 FROM N.A.
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563 AA; 6
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30 RELSEOI 36

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MOES MOUSE
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SEQUENCE
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MOES_MOUSE
à
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"Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides.";
Spectrometric identification of sorted N-terminal peptides.";
Nat. Biotechnol. 21:566-569(2003).
Is EVINCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-: FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-: TISSUE SPECIFICITY: In all tissues and cultured cells studied.
-: TISSUE SPECIFICITY: In all tissues and cultured cells studied.
-: SIMILARITY: Contains I FERM domain.
-: DATABASE: NAME=Atias Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/WSNID363.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-2238627; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlansner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blachenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Morley K.C., Halle S., Gazcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Richards S., Worley K.C., Halle S., Gazcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                       Lankes W.T., Furthmayr H.; "Moesin: a member of the protein 4.1-talin-ezrin family of proteins."; Proc. Natl. Acad. Sci. U.S.A. 88:8297-8301(1991).
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1-15; 53-59 AND 413-434
                                                                                                                                                                                                                                                                                                                                                                                                                                           Howden P.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                      MEDLINE=92020840; PubMed=1924289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences.
                                                                                                     STANDARD;
 315 RELSEQI 321
                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Pancreas;
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                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
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                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                     MOES HUMAN
                                                                   RESULT 14
MOES_HUMAN
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
STRAINE-NOD; TISSUE-Thymus;
MEDLINE-22354683; PubMed=12466851;
MEDLINE-22354683; PubMed=12466851;
OKAZAKI Y., FURTHON, KASHKAWA T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Nikaido I., Osato N., Saito R., Suzuki H., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO: 0005886; C: Cytoskeleton; TAS.
GO; GO: 0005886; C: Cytoskeleton; TAS.
GO; GO: 0005280; F: structural constituent of cytoskeleton; TAS.
InterPro; IPR000799; Band 4.1.
InterPro; IPR000799; Bar/rad/moesin.
R InterPro; IPR000799; Band 4.1.
R InterPro; IPR000799; Band 4.1.
R Pfan; PF00737; Band 4.1; I.
R Pfan; PF00759; ERM; I.
R RAINTS; PR00335; BAND41.
R SMART; SM00295; B41; I.
R ROSITE; PS00660; PERM 1; I.
R PROSITE; PS00660; PERM 2; I.
R PROSITE; PS00661; PERM 2; I.
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Sato N., Funayama N., Nagafuchi A., Yonemura S., Tsukita S.,
Tsukita S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 576;
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576 AA; 67689 MW; 96CE7C28D55A8176 CRC64;
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01-FRB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Moesin (Membrane-organizing extension spike protein)
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INIT_MET 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 7; DB 1; 100.0%; Pred. No. 14; ative 0; Mismatches
                                                                                                                                                                                                                                                                                       Aarhus/Ghent-2DPAGE; 3515; IEF.
Aarhus/Ghent-2DPAGE; 3516; IEF.
Genew; HGNC:7373; MSN.
MIM; 309845;
                                                                                                                                                                 EMBL, BC017293; AAH17293.1; -. BIR, A41289; AA1289. AA1289. BEB. 1ESW; 27-JUN.01. PDB; 1EF1; 10-MAY-00.
                                                                                                    EMBL; M69066; AAA36322.1; -.
EMBL; Z98946; CAB46379.1; -.
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Best Local Similarity luv..
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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RADILINE-228825; PubMed=12477922;

RA STRAIN=FVB/N; TISSUE=Breast tumor;

RX STRAIN=FVB/N; TISSUE=Breast tumor;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.H.,

RA Nilalon D.K., Murny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

RA Hakesley N., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length

Physical Research A., Schein J.L., Schoolfoolt.)
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
A Kanaj A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I. W., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
A Suleana R., Takenaka Y., Taylor M.S., Teasdale R.D., Temita M.,
Verardo R., Wanshaw-Boiis A., Yanagisawa M., Yang L.,
Wilming L.G., Wynshaw-Boiis A., Yanagisawa M., Yang L.,
Xuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
A Hirozane C., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Vernich A., Verkin, N., Sasaki D., Shibara K., Shinagawa A.,
Verkich A., Verkin, N., Verkin, N., Nerkin, N.,
Verkinich A., Verkin, N., Sasaki D., Shibara K., Shinagawa A.,
Verkinich A., Verkin, N., Nerkin, N., Sanaki D.,
Verkinich A., Verkin, N., Nerkin, N.,
Verkin, N., Nerkin, N., Nerkin, N.,
Verkin, N., Nerkin, N., Nerkin, N.,
Verkin, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.,
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILNE=92243764; PubMed=1573844;
MEDILNE=92243764; PubMed=1573844;
Furthmayr H., Lankes W.T., Amieva M.R.;
Furthmayr H., Lankes W.T., Amieva M.R.;
Fuchimayr H., Enchell protein and constituent of filopodia: its
role in cellular functions.";
Kidney Int. 41:665-670(1992).
-!- FUNCTION: Probably involved in connections of major cytoskeletal
structures to the plasma membrane.
-!- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MGD; MGI:97167; Msn. InterPro; PR000029B; Band 4.1. InterPro; IPR00099B; Ez/rad/moesin. InterPro; IPR008954; Moesin.

PF00373; Band 41; 1

EMBL; AK088336; BAC40290.1; -. EMBL; BC047366; AAH47366.1; -. M86390; AAA39728.1; -.

EMBL;

EMBL; S47577; AAA11762.1;

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Gaps
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0
                                                                                                                           Length 576;
                                                                                                                                               0; Indels
                                                                                   EL.... DV (IN REF. 4).
RA -> SP (IN REF. 4).
5E0F455552E9145 CRC64;
                                                                                                                            DB 1;
                            PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00657; FERM 3; 1.
Structural protein; Cytoskeleton.
INIT_MET 0 0 BY SIMILARITY.
                                                                                                                            Score 7; DB 1;
Pred. No. 14;
                                                                                                                                    100.0%; Pred. No. -
                                                                                                                                                                                                            completed: August 16, 2004, 09:55:16
ne : 33 secs
                                                                              FERM.
                                                                                                          67635 MW;
                                                                                                                             17.18;
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Pfam; PF00769; ERM; 1.
PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                      341 REKEELM 347
                                                                                                                                                                    9 REKEELM 15
                                                                                                         576 AA;
                                                                                      330
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August 16, 2004, 09:52:37; Search time 36 Seconds (without alignments) 359.340 Million cell updates/sec
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1 EREKEÇMMREKEELMLRLÇD.......EEKTKKAERELSEÇIQRALQ 41
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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sp_bacteria:*
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

Description	homo	Qyujza nomo sapien Q9ujz8 homo sapien	Q9uk20 homo sapien	Q9ujz2 homo sapien	Q8cbu4 mus musculu	Q8vhk3 rattus norv	Q89k2l bradyrhizob	Q9g103 sus scrofa	Q8suw1 encephalito	Q9zew2 enterobacte	Q56576 vibrio algi	Q9c673 arabidopsis	Q9brx7 homo sapien	0975al sulfolobus	Q8wv17 homo sapien
SUMMARIES	090027	09UJZ6 09UJZ8	Q9UK20	Q9UJZ2	Q8CBU4	Q8VHK3	Q89K21	Q9GL03	QBSUW1	Q9ZEW2	Q56576	Q9C673	Q9BRX7	7 Q975A1	Q8WV17
DB	4.	4, 4,	4	4	11	11	16	9	ហ	7	7	10	4	17	4
% Query Match Length DB	158	159	161	152	421	455	547	578	901	65	128	142	146	181	195
% Query Match	8.8	4.8 8.8 8.6	46.3	43.9	29.3	29.3	19.5	19.5	19.5	17.1	17.1	17.1	17.1	17.1	17.1
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7 17.1 266 4 09H611 7 17.1 266 16 08ZM57 7 17.1 267 16 07UET6 7 17.1 267 11 08BA72 7 17.1 303 17 097UM3 7 17.1 309 11 08CZT7 7 17.1 309 11 08EXV8 7 17.1 428 16 083CO0 7 17.1 452 3 08B83 7 17.1 490 4 07ZSQ9 7 17.1 490 4 07ZSQ9 7 17.1 491 4 07ZSQ9 7 17.1 491 4 07ZSQ9 7 17.1 501 11 09D0C4	17.1 521 11 17.1 586 15 17.1 586 15 17.1 581 16 17.1 622 16 17.1 627 11 17.1 650 11 17.1 650 11 17.1 650 11 17.1 650 11 17.1 650 11 17.1 668 16
11 118 118 222 224 226 228 309 310	0.000000000000000000000000000000000000

ALIGNMENTS

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RESULT 1

090127

AC 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-TAN-2003 (TrEMBLrel. 24, Last annotation update)
DT 01-TAN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ezini (Fragment).
DE EZINI (Fragment).
C Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammaliaja Eutheria; Primates; Catarrhini; Hominidae; Homo.
C Mammalia; Expensive Expression; Expression;
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137 EREKEÇMIRENEBLIMLIKLIZ 20

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RESULT 2 Q9UJZ6

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                 No. 14]

No. 14]

C. TISSUE=Placenta;

A. Chen Z.C., Fadiel A., Naftolin F.;

Chen Z.C., Fadiel A., Naftolin F.;

Chen Z.C., Fadiel A., Naftolin F.;

Chen Z.C., Fadiel B., Naftolin F.;

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AF187552; AAD56713.1;

R. GO; GO: 0005856; C: Cytoskeleton; IEA.

R. InterPro; IPR000799; Band 4.1.

R. Prostre; PSF00759; EZ/xad/moesin.

R. Pfam; PF00769; ERM; 1.

R. PROSITE; PS50657; FERM, 3; 1.

R. NON TER.

1 1 100 TER.

1 1 161

SEQÜENCE 161 AA; 19439 MW; SFD6EB910E017099 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen Z.C., Fadiel A., Naftolin F.;

"Mutation of cytovillin gene in glioblastoma.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AT190059; AAF03158 11;

GO; GO:0005856; C:Cytoskeleton; IEA.

R InterPro; IPR000299; Band 4.1.

R InterPro; IPR000799; Ez/rād/moesin.

R PF6an; PF00769; ERFM, 1.

R PROSITE; PS50057; FERM, 3; 1.

R NON TER

I ST 152

SEQÜENCE 152 AA; 18416 MW; B7FCE817DD2B9291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%; Score 18; DB 4; Length 152; 100.0%; Pred. No. 2.6e-10; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MNY-2000 (TrEMBLrel. 13, Created)
01-MNY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytovillin 2 (Fragment).
              QUXZO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UND-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment).
161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 100.0
Matches 18; Conservative
PRELIMINARY;
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                                                                                                                   Homo sapiens (Human)
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TISSUE=Brain;
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  29UK20
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Q1-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Ezrin (Fragment).

Ezrin (Fragment).

Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 46.3%; Score 19; DB 4; Length 156; Local Similarity 100.0%; Pred. No. 2.6e-11; nes 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Z.C., Fadiel A., Naftolin F.;
"Mutation of ezrin gene in cancer.";
submitted (SEP-199) to the EMBL/GenBank/DDBJ databases.
EMBL, AF188895; AR701154.1; -.
GO; GO:0005856; C:cytoskeleton; IEA.
InterPro; IRR000799; Band_4.1.
InterPro; IRR000799; Ez/rad/moesin.
PROSITE; PS50057; FERM_3; 1.
                                                                                                                                                                                                         Fadiel A., Chen Z.C., Naftolin F.;
Fadiel A., Chen Z.C., Naftolin F.;
"Mutation of earin gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF189213; AAF03156.1; -.
EMBL; AF189213; AAF03156.1; -.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000799; Ea/rad/moesin.
Pfam; PF00769; ERM; 1.
PROSITE; PS50057; FERM, 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               159 159 AA; 19234 MW; 7C398388B7BA70FA CRC64;
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156 156
156 AA; 19042 MW; 159F5AA684A2C3A6 CRC64;
                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment)
    159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 156 AA.
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 EREKEÇMMREKEELMLRLQD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EREKEOMMREKEELMLRLQD 20
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    PRELIMINARY;
                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                          NCBI_TaxID=9606;
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NON TER
SEQUENCE
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NON TER
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Matches 20;
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Q9UJZ8

RESULT 3 92UU60

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Gaps

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RESULT 4 Q9UK20

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Best Loca Matches

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Gaps

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134 EREKEOMMREKEELMLRL 151

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9 REKEELMIRLOD 20
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                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 KAERELSE 34
  455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Q9GL03
                                                                                                                                                                                                                                                RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
while I be a consortium of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
Nature 420:563-573 (2002).
InterPro; PR000299; PR000299; Band_4.1.
InterPro; IPR000299; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.3%; Score 12; DB 11; Length 421; 100.0%; Pred. No. 0.00063; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;

Gunn-Moore F.J., Tait S., Brophy P.J.;

Submitred (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF45c298 AAL47944.1;

GO, GO.0058856; C:cytoskeleton; IEA.

InterPro; IPR000299; Band 4.1.

InterPro; IPR000798; Ez/rād/moesin.

Pfam; PF0073; Band 4.1.

Pfam; PF00769; ERM; 1.

PRINTS; PR00955; BAND11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 AA; 50273 MW; E8D6C0D03F6E7497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                          Last sequence update)
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                                                                 421 AA
                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Urinary bladder; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                        Created)
                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Pfam; PF00769; ERN, 1.
PROSITE; PS00661; FERM_2; 1.
PROSITE; PS50057; FERM_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR 2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24, Ezrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
                                                                                                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Villin 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 REKEELMLRLQD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 REKEELMLRLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00295; B41;
                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                           Q8CBU4
ID Q8CBU4
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0804HX3
1D 0804HX3
1D 01-M
DT 01-M
DT 01-T
DE Exrip
OC Buka
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                        RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005953; BAC5022.1; --
GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR006089; Acyl-CoA_dh.
InterPro; IPR006090; Acyl-CoA_dh.
InterPro; IPR006091; Acyl-CoA_dh.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
[1]
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Aryl CoA bliso97.
Bradyrhizobium japonicum.
Bacteria; Proteobacteria: Alphaproteobacteria; Rhizobiales;
                                                      29.3%; Score 12; DB 11; Length 455; 100.0%; Pred. No. 0.00067; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 AA; 59318 MW; 62C18C6DDA7B1F6F CRC64;
54174 MW; 1FC9A95F4C7D5893 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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19.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches
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Pfam, PF00470; Acyl-CoA_dh_M, 1.
PROSITE; PS00072; ACYL_COA_DH_1.
PROSITE; PS00073; ACYL_COA_DH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bradyrhizobiaceae; Bradyrhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Period protein (Fragment).
                                                                                                                                                                                                                                       342 REKEELMIRLOD 353
                                                             Query Match 29.3
Best Local Similarity 100.
Matches 12; Conservative
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65 AA

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STRAIN=B138-2;
MEDLINE=96332623; PubMed=8695633;
                                                       01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2003 (TrEMBLrel. 24, COpB (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                          Enterobacter intermedius.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ERELSEQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 ERELSEQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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                          STRAINE-FROM N.A.

SKINNET T.M., Anderson S.I., Lopez-Corrales N.L., Loudon A.S.,
Haley C.S., Archibald A.L.;
Haley C.S., Archibald A.L.;
Haley C.S., Archibald A.L.;
Genetic and physical mapping, expression analysis and partial gene
or genence of portine Perl.";
Sequence of portine Perl.";
Sept. A.Z77735; CAC15393.1;
CO; GO:000415; P:Signal transduction; IEA.

O; GO:0004165; P:Signal transduction; IEA.

InterPro; IPR00489; PAS; 1.

SWART; SM00091; PAS; 1.

SWART; SM00091; PAS; 1.

SWART; SM00091; PAS; 1.

SWART; PSS0112; PAS; 1.

SWART; SW00091; PAS; 1.
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Katinka M.D., Duprat S., Cormillot E., Metenier G., Thomarat F.,

Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,

Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,

Weissenbach J., Vivares C.P.;

Welcenne sequence and gene compaction of the eukaryote parasite

Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Encephalitozoon cuniculi.
Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
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GO; GO:0003735; F:structural constituent of ribosome; IEA.
Ribosomal protein; Hypothetical protein.
SEQUENCE 901 AA; 96503 MW; 37C2D28ABF2F3A92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%; Score 8; DB 5; Length 901; 100.0%; Pred. No. 12; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 AA; 62238 MW; 9A80CF55885E32AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBSUM1;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ECU07_1530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.5%; Score 8; DB 6;
100.0%; Pred. No. 8.4;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 ELSEQIÓR 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 EEKTKKAE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 ELSEQIOR 38
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
Q8SUW1
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ACCOCO OCT STANDACT S

RESULT 11 29ZEW2

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STRAIN=AH14;
MEDLINE=20431899; PubMed=10974114;
OSDOIN A.W., Da Silva Tatley F.M., Steyn L.M., Pickup R.W.,
Saunders U.R.;
"Mosaic plasmids and mosaic replicons: evolutionary lessons from the analysis of genetic diversity in IncFII-related replicons.";
Microbiology 146:2267-2275 (2000).
Microbiology 146:2267-2275 (2000).
GO: 0046821; C.extrachromosomal DNA; IEA.
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                                                                                                                                                                                                                                     Plasmid pLV1402.
Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
NCBI_TaxID=61648;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 55, Last annotation update)
Multifunctional regulator of fatty acid metabolism (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio alginolyticus.
Bateria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 65;
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SMART; SM00345; HTH GNTR; 1.
PROSITE; PS00043; HTH GNTR; 1.
DNA-binding; Transcription; Transcription regulation.
NON TER 128 AB: 14.4.
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Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 14;
tive 0; Mismatches
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Search completed: August 16, 2004, 09:56:03
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein ST0512.
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[1]
SEQUENCE FROM N.A.
TISSUE=Brain, and Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 10...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 EKEELML 143
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Hypothetical protein
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wes 7; Conserv
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MEDLINE-21016719; PubMed=11130712;

MEDLINE-21016719; PubMed=11130712;

MEDLINE-21016719; PubMed=11130712;

MEDLINE-21016719; PubMed=11130712;

MICO., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Munter O., Alonso J., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Honsen N.F., Hughes B., Huizar L.,

All J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khapkin B.,

And C.J., Koo H.L., Kreenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lanz C.A., Li J.H., Li Y.-B.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nechman W.C., Osborne B.I.,

Pai G., Peterson J., Pham P.K., Rizzo M., Ronney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Pai G., Peterson J., Tambunga G., Toriumi M.J., Town C.D.,

Wu Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                   Gaps
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                         Length 128;
                                                                   0; Indels
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PIR; C86389; O86389.
Hypotheticlal protein.
SEQUENCE 142 AA; 17315 MW; 4DD3225FD6D60997 CRC64;
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01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Histone deacetylase 6)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
           17.1%; Sco...
100.0%; Pred. No. ...
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                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                             28 AERELSE 34
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Q9BRX7
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090673
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Crenarchaeon, Sulfolobus tokodaii strain7.";

ENBL, Apo00982; Bab65506.1;

GO, GO00887; Finucleic acid binding; IEA.
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                                                                           SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Kaudinga M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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181 AA; 20506 MW; 189F3BC6D019FF55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16399 MW; 6A2C1261CE1F83EB CRC64;
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Last annotation update)
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100.0%; Pred. No. 27;
iive 0; Mismatches
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Pred. No.
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Job time : 37 secs

Mon Aug 16 10:46:51 2004